

SEQUENCE LISTING

<110> Gaiger, Alexander  
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 Corixa Corporation

<120> Compositions and Methods for the Detection, Diagnosis  
 and Therapy of Hematological Malignancies

<130> 014058-014402PC

<140> WO PCT/US03/02353

<141> 2003-01-22

<150> US 10/057,475

<151> 2002-01-22

<160> 124

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Homo sapiens

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Lys Asn Asp Ser Gly Ile Tyr Tyr Val Gly Ile Tyr Ser Ser Ser Leu
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Ser Lys Pro Lys Val Thr Met Gly Leu Gln Ser Asn Lys Asn Gly Thr
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Cys Val Thr Asn Leu Thr Cys Cys Met Glu His Gly Glu Glu Asp Val
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Gly Ser Ile Leu Pro Ile Ser Trp Arg Trp Gly Glu Ser Asp Met Thr
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Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser  
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Cys Arg Glu Met Ala Gly Ser Gly Thr Cys Gly Thr Val Val Ser Thr  
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Thr Asn Phe Ile Lys Ala Glu Tyr Lys Gly Arg Val Thr Leu Lys Gln  
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Tyr Pro Arg Lys Asn Leu Phe Leu Val Glu Val Thr Gln Leu Thr Glu  
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Ser Asp Ser Gly Val Tyr Ala Cys Gly Ala Gly Met Asn Thr Asp Arg  
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Gly Lys Thr Gln Lys Val Thr Leu Asn Val His Ser Glu Tyr Glu Pro  
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Ser Trp Glu Glu Gln Pro Met Pro Glu Thr Pro Lys Trp Phe His Leu  
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Pro Tyr Leu Phe Gln Met Pro Ala Tyr Ala Ser Ser Ser Lys Phe Val  
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Thr Arg Val Thr Thr Pro Ala Gln Arg Gly Lys Val Pro Pro Val His  
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His Ser Ser Pro Thr Thr Gln Ile Thr His Arg Pro Arg Val Ser Arg  
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Ala Ser Ser Val Ala Gly Asp Lys Pro Arg Thr Phe Leu Pro Ser Thr  
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Thr Ala Ser Lys Ile Ser Ala Leu Glu Gly Leu Leu Lys Pro Gln Thr  
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Pro Ser Tyr Asn His His Thr Arg Leu His Arg Gln Arg Ala Leu Asp  
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Tyr Gly Ser Gln Ser Gly Arg Glu Gly Gln Gly Phe His Ile Leu Ile  
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Pro Thr Ile Leu Gly Leu Phe Leu Leu Ala Leu Leu Gly Leu Val Val  
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Lys Arg Ala Val Glu Arg Arg Lys Ala Leu Ser Arg Arg Ala Arg Arg  
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Leu Ala Val Arg Met Arg Ala Leu Glu Ser Ser Gln Arg Pro Arg Gly  
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 Arg Ala Arg Gly Ala Asp Ala Ala Gly Thr Gly Glu Ala Pro Val Pro  
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 Pro Trp Leu His Ala Pro Ser Leu Lys Thr Ser Cys Glu Tyr Val Ser  
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reading frame His tag fusion

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reading frame His tag fusion

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      35              40              45

Leu Asp Ile Arg Leu Met Arg His Lys Ala Val Trp Ile Asn Pro Gln
      50              55              60

Asp Val Gln Gln Gln Pro Gln Asp Leu Gln Ser Gln Val Pro Ala Ala
      65              70              75              80

Gly Asn Ser Gly Thr His Phe Val Thr Asp Ala Ala Ser Pro Ser Gly
      85              90              95

Pro Ser Pro Ser Cys Leu Gly Asp Ser Leu Ala Glu Thr Thr Leu Ser
      100              105              110

Glu Asp Thr Thr Asp Ser Val Gly Ser Ala Ser Pro His Gly Ser Ser
      115              120              125

Glu Lys Ser Ser Ser Phe Ser Leu Ser Ser Thr Glu Val His Met Val
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Arg Pro Gly Tyr Ser His Arg Val Ser Leu Pro Thr Ser Pro Gly Ile
      145              150              155              160

Leu Ala Thr Ser Pro Tyr Pro Glu Thr Asp Ser Ala Phe Phe Glu Pro
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Ser His Leu Thr Ser Ala Ala Asp Glu Gly Ala Val Gln Val Ser Arg
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Arg Thr Ile Ser Ser Asn Ser Phe Ser Pro Glu Val Phe Val Leu Pro
      195              200              205

Val Asp Val Glu Lys Glu Asn Ala His Phe Tyr Val Ala Asp Met Ile
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Ile Ser Ala Met Glu Lys Met Lys Cys Asn Ile Leu Ser Gln Gln Gln
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<211> 662

<212> PRT

<213> Homo sapiens

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Leu Asn Thr Asp His Pro Pro Cys Gln Leu Asp Ile Arg Leu Met Arg
 35             40             45

His Lys Ala Val Trp Ile Asn Pro Gln Asp Val Gln Gln Gln Pro Gln
 50             55             60

Asp Leu Gln Ser Gln Val Pro Ala Ala Gly Asn Ser Gly Thr His Phe
 65             70             75             80

Val Thr Asp Ala Ala Ser Pro Ser Gly Pro Ser Pro Ser Cys Leu Gly
 85             90             95

Asp Ser Leu Ala Glu Thr Thr Leu Ser Glu Asp Thr Thr Asp Ser Val
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Gly Ser Ala Ser Pro His Gly Ser Ser Glu Lys Ser Ser Ser Phe Ser
115            120            125

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 <212> PRT  
 <213> Homo sapiens

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  20              25              30

Leu Asn Thr Asp His Pro Pro Cys Gln Leu Asp Ile Arg Leu Met Arg
  35              40              45

His Lys Ala Val Trp Ile Asn Pro Gln Asp Val Gln Gln Gln Pro Gln
  50              55              60

Asp Leu Gln Ser Gln Val Pro Ala Ala Gly Asn Ser Gly Thr His Phe
  65              70              75              80

Val Thr Asp Ala Ala Ser Pro Ser Gly Pro Ser Pro Ser Cys Leu Gly
  85              90              95

Asp Ser Leu Ala Glu Thr Thr Leu Ser Glu Asp Thr Thr Asp Ser Val
  100             105             110

Gly Ser Ala Ser Pro His Gly Ser Ser Glu Lys Ser Ser Ser Phe Ser
  115             120             125

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Leu	Ser	Ser	Thr	Glu	Val	His	Met	Val	Arg	Pro	Gly	Tyr	Ser	His	Arg	130	135	140
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Glu	Thr	Asp	Ser	Ala	Phe	Phe	Glu	Pro	Ser	His	Leu	Thr	Ser	Ala	Ala	165	170	175
Asp	Glu	Gly	Ala	Val	Gln	Val	Ser	Arg	Arg	Thr	Ile	Ser	Ser	Asn	Ser	180	185	190
Phe	Ser	Pro	Glu	Val	Phe	Val	Leu	Pro	Val	Asp	Val	Glu	Lys	Glu	Asn	195	200	205
Ala	His	Phe	Tyr	Val	Ala	Asp	Met	Ile	Ile	Ser	Ala	Met	Glu	Lys	Met	210	215	220
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<211> 1033

<212> PRT

<213> Homo sapiens

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Lys	Ile	Ile	Asn	Cys	Leu	Ser	Ser	Gly	Lys	Trp	Ser	Ala	Val	Pro	Pro
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 Thr Ser Asn Asp Gln Glu Arg Gly Thr Trp Ser Gly Pro Ala Pro Leu  
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Cys Lys Leu Ser Leu Leu Ala Val Gln Cys Ser His Val His Ile Ala  
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 Pro Ala Gly Ser Arg Val Glu Leu Val Asn Thr Ser Cys Gln Asp Gly  
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Ser Ser Pro Ala Asp Met Asp Gly Ile Gln Lys Gly Leu Glu Pro Arg  
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Tyr Met Leu Glu Gly Ser Pro Gln Ser Gln Cys Gln Ser Asp His Gln  
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Ala	Val	Gly	Gln	Leu	Gly	Val	Arg	Val	Phe	His	Ser	Ser	Pro	Ala	Ala	35	40	45	
Ser	Ser	Leu	Asp	Phe	Ile	Gly	Gly	Pro	Ala	Ile	Leu	Leu	Gly	Leu	Ile	50	55	60	
Ser	Leu	Ala	Thr	Asp	Asp	His	Thr	Met	Tyr	Ala	Ala	Val	Lys	Val	Leu	65	70	75	80
His	Ser	Val	Leu	Thr	Ser	Asn	Ala	Met	Cys	Asp	Phe	Leu	Met	Gln	His	85	90	95	
Ile	Cys	Gly	Tyr	Gln	Ile	Met	Ala	Phe	Leu	Leu	Arg	Lys	Lys	Ala	Ser	100	105	110	
Leu	Leu	Asn	His	Arg	Ile	Phe	Gln	Leu	Ile	Leu	Ser	Val	Ala	Gly	Thr	115	120	125	
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Gln	His	Ile	Leu	Cys	Asn	Phe	Glu	Leu	Trp	Met	Asn	Thr	Ala	Asp	Asn	145	150	155	160
Leu	Glu	Leu	Ser	Leu	Phe	Ser	His	Leu	Leu	Glu	Ile	Leu	Gln	Ser	Pro	165	170	175	
Arg	Glu	Gly	Pro	Arg	Asn	Ala	Glu	Ala	Ala	His	Gln	Ala	Gln	Leu	Ile	180	185	190	
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Lys	Pro	Ser	Ser	Val	Asn	Glu	Arg	Gln	Ile	Cys	Met	Asp	Gly	Ala	Leu	245	250	255	
Asp	Pro	Ser	Leu	Pro	Ala	Gly	Ser	Gln	Thr	Ser	Gly	Lys	Thr	Ile	Trp	260	265	270	

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Ser Gln Gln Lys Arg Asp Phe Gln Ser Glu Val Leu Leu Ser Ala Met  
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 Glu Leu Phe His Met Thr Ser Gly Gly Asp Ala Ala Met Phe Arg Asp  
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 Gly Lys Glu Pro Gln Pro Ser Ala Glu Ala Ala Ala Pro Ser Leu  
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 Gly Met Phe Ser Ala Asp Pro Arg His Ile Leu Leu Phe Ile Leu Glu  
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 His Ile Met Val Val Ile Glu Thr Ala Ser Ser Gln Arg Asp Thr Val  
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 Leu Ser Thr Leu Tyr Ser Ser Leu Asn Lys Val Ile Leu Tyr Cys Leu  
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 Ser Lys Pro Gln Gln Ser Leu Ser Glu Cys Leu Gly Leu Leu Ser Ile  
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 Leu Gly Phe Leu Gln Glu His Trp Asp Val Val Phe Ala Thr Tyr Asn  
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 Ser Asn Ile Ser Phe Leu Leu Cys Leu Met His Cys Leu Leu Leu Leu  
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 Met Ser Thr Tyr His Gln Val Phe Leu Ser Pro Asn Glu Asp Val Lys  
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 Glu Lys Arg Glu Asp Leu Pro Ser Leu Ser Asp Val Gln His Asn Ile  
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1569

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Asp	Tyr	Ser	Asn	Trp	Ala	Pro	Gly	Glu	Pro	Thr	Ser	Arg	Ser	Gln	Gly	
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Glu	Asp	Cys	Val	Met	Met	Arg	Gly	Ser	Gly	Arg	Trp	Asn	Asp	Ala	Phe	
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Cys Asp Arg Lys Leu Gly Ala Trp Val Cys Asp Arg Leu Ala Thr Cys  
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 Arg Pro Asp Pro Asp Gly Arg Leu Pro Thr Pro Ser Ala Pro Leu His  
 305 310 315 320

Ser

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<211> 568

<212> PRT

<213> Homo sapiens

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Val Pro Glu Asp Leu Ser Thr Thr Ser Gly Ala Gln Gln Asn Ser Lys  
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Ser Asp Arg Gly Met Ala Ser Asn Val Lys Val Glu Thr Gln Ser Asp  
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Glu Glu Asn Gly Arg Ala Cys Glu Met Asn Gly Glu Glu Cys Ala Glu  
65 70 75 80  
Asp Leu Arg Met Leu Asp Ala Ser Gly Glu Lys Met Asn Gly Ser His  
85 90 95  
Arg Asp Gln Gly Ser Ser Ala Leu Ser Gly Val Gly Gly Ile Arg Leu  
100 105 110  
Pro Asn Gly Lys Leu Lys Cys Asp Ile Cys Gly Ile Val Cys Ile Gly  
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Pro Asn Val Leu Met Val His Lys Arg Ser His Thr Gly Glu Arg Pro  
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Phe Gln Cys Asn Gln Cys Ser Ser Ala Leu Ser Gly Val Gly Gly Ile  
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Ile Gly Pro Asn Val Leu Met Val His Lys Arg Ser His Thr Gly Glu  
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Arg Pro Phe Gln Cys Asn Gln Cys Gly Ala Ser Phe Thr Gln Lys Gly  
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Cys His Leu Cys Asn Tyr Ala Cys Arg Arg Arg Asp Ala Leu Thr Gly  
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Cys His Asn Tyr Leu Glu Ser Met Gly Leu Pro Gly Met Tyr Pro Val  
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Ala Lys Arg Lys Ser Ser Met Pro Gln Lys Phe Leu Gly Asp Lys Cys  
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 Gly Glu His Arg Tyr His Leu Ser  
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 <211> 350  
 <212> DNA  
 <213> Homo sapiens

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<210> 29

<211> 191

<212> PRT

<213> Homo sapiens

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Thr Leu Ile Trp Arg Leu Phe Phe Leu Ile Met Phe Leu Thr Ile Ile
 35             40             45

Val Cys Gly Met Val Ala Ala Leu Ser Ala Ile Arg Ala Asn Cys His
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Gln Glu Pro Ser Val Cys Leu Gln Ala Ala Cys Pro Glu Ser Trp Ile
 65             70             75             80

Gly Phe Gln Arg Lys Cys Phe Tyr Phe Ser Asp Asp Thr Lys Asn Trp
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Thr Ser Ser Gln Arg Phe Cys Asp Ser Gln Asp Ala Asp Leu Ala Gln
 100            105            110

Val Glu Ser Phe Gln Glu Leu Asn Phe Leu Leu Arg Tyr Lys Gly Pro
 115            120            125

Ser Asp His Trp Ile Gly Leu Ser Arg Glu Gln Gly Gln Pro Trp Lys
 130            135            140

Trp Ile Asn Gly Thr Glu Trp Thr Arg Gln Phe Pro Ile Leu Gly Ala
 145            150            155            160

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 50 55 60  
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 Pro Gly Val Ile Arg Leu Leu Asp Trp Phe Glu Thr Gln Glu Gly Phe  
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 245 250 255  
 Pro Asp Cys Cys Ala Leu Ile Arg Arg Cys Leu Ala Pro Lys Pro Ser  
 260 265 270

Ser Arg Pro Ser Leu Glu Glu Ile Leu Leu Asp Pro Trp Met Gln Thr  
275 280 285

Pro Ala Glu Asp Val Thr Pro Gln Pro Leu Gln Arg Arg Pro Cys Pro  
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Phe Gly Leu Val Leu Ala Thr Leu Ser Leu Ala Trp Pro Gly Leu Ala  
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<212> DNA  
<213> Homo sapiens

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cagaaactgt attttcatct cagcctagtg acgatgaatc aagtagtgat gaaaccagta 720  
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<210> 35

<211> 755

<212> PRT

<213> Homo sapiens

<400> 35

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      20              25              30

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Thr Asp Ser Cys Glu Pro Ala Pro Glu Cys Ser Ser Leu Glu Gln Glu
      35              40              45

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Glu Leu Gln Ala Leu Gln Ile Glu Gln Gly Glu Ser Ser Gln Asn Gly
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Thr	Val	Leu	Met	Glu	Glu	Thr	Ala	Tyr	Pro	Ala	Leu	Glu	Glu	Thr	Ser	65	70	75	80
Ser	Thr	Ile	Glu	Ala	Glu	Glu	Gln	Lys	Ile	Pro	Glu	Asp	Ser	Ile	Tyr	85	90	95	
Ile	Gly	Thr	Ala	Ser	Asp	Asp	Ser	Asp	Ile	Val	Thr	Leu	Glu	Pro	Pro	100	105	110	
Lys	Leu	Glu	Glu	Ile	Gly	Asn	Gln	Glu	Val	Val	Ile	Val	Glu	Glu	Ala	115	120	125	
Gln	Ser	Ser	Glu	Asp	Phe	Asn	Met	Gly	Ser	Ser	Ser	Ser	Ser	Gln	Tyr	130	135	140	
Thr	Phe	Cys	Gln	Pro	Glu	Thr	Val	Phe	Ser	Ser	Gln	Pro	Ser	Asp	Asp	145	150	155	160
Glu	Ser	Ser	Ser	Asp	Glu	Thr	Ser	Asn	Gln	Pro	Ser	Pro	Ala	Phe	Arg	165	170	175	
Arg	Arg	Arg	Ala	Arg	Lys	Lys	Thr	Val	Ser	Ala	Ser	Glu	Ser	Glu	Asp	180	185	190	
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Arg	Gln	Phe	Ser	Ser	Gly	Leu	Asn	Lys	Cys	Val	Ile	Leu	Ala	Leu	Val	210	215	220	
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Gln	Lys	Arg	Gln	Gln	Leu	Val	Arg	Lys	Ile	His	Glu	Asp	Glu	Leu	Asn	245	250	255	
Asp	Met	Lys	Asp	Tyr	Leu	Ser	Gln	Cys	Gln	Gln	Glu	Gln	Glu	Ser	Phe	260	265	270	
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Thr	Glu	Asn	Gln	Tyr	Leu	Arg	Val	Ser	Leu	Glu	Lys	Glu	Glu	Lys	Ala	305	310	315	320
Leu	Ser	Ser	Leu	Gln	Glu	Glu	Leu	Asn	Lys	Leu	Arg	Glu	Gln	Ile	Arg	325	330	335	
Ile	Leu	Glu	Asp	Lys	Gly	Thr	Ser	Thr	Glu	Leu	Val	Lys	Glu	Asn	Gln	340	345	350	
Lys	Leu	Lys	Gln	His	Leu	Glu	Glu	Glu	Lys	Gln	Lys	Lys	His	Ser	Phe	355	360	365	
Leu	Ser	Gln	Arg	Glu	Thr	Leu	Leu	Thr	Glu	Ala	Lys	Met	Leu	Lys	Arg	370	375	380	

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 385 390 395 400  
 Gln Gln Leu Ser Gly Ser Gln Leu His Gly Lys Ser Asp Ser Pro Asn  
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 Val Tyr Thr Glu Lys Lys Glu Ile Ala Ile Leu Arg Glu Arg Leu Thr  
 420 425 430  
 Glu Leu Glu Arg Lys Leu Thr Phe Glu Gln Gln Arg Ser Asp Leu Trp  
 435 440 445  
 Glu Arg Leu Tyr Val Glu Ala Lys Asp Gln Asn Gly Lys Gln Gly Thr  
 450 455 460  
 Asp Gly Lys Lys Lys Gly Gly Arg Gly Ser His Arg Ala Lys Asn Lys  
 465 470 475 480  
 Ser Lys Glu Thr Phe Leu Gly Ser Val Lys Glu Thr Phe Asp Ala Met  
 485 490 495  
 Lys Asn Ser Thr Lys Glu Phe Val Arg His His Lys Glu Lys Ile Lys  
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 515 520 525  
 Val Lys Ser Thr Phe Arg His Phe Lys Asp Thr Thr Lys Asn Ile Phe  
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 Lys Pro Arg Thr Val Phe Ser Asp Tyr Leu His Pro Gln Tyr Lys Ala  
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 Pro Thr Glu Asn His Ser Arg Pro Tyr Tyr Ala Lys Arg Trp Lys Glu  
 580 585 590  
 Glu Lys Pro Val His Phe Lys Glu Phe Arg Lys Asn Thr Asn Ser Lys  
 595 600 605  
 Lys Cys Ser Pro Gly His Asp Cys Arg Glu Asn Ser His Ser Phe Arg  
 610 615 620  
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 625 630 635 640  
 Leu Phe Asn Thr Val Val Ile Pro Ile Arg Met Asp Glu Phe Arg Gln  
 645 650 655  
 Ile Ile Gln Arg Tyr Met Leu Lys Glu Leu Asp Thr Phe Cys Arg Trp  
 660 665 670  
 Asn Glu Leu Asp Gln Phe Ile Asn Lys Phe Phe Leu Asn Gly Val Phe  
 675 680 685  
 Ile His Asp Gln Lys Leu Phe Thr Asp Phe Val Asn Asp Val Lys Ile  
 690 695 700

Ile Leu Gly Asn Met Lys Glu Tyr Glu Val Asp Asn Asp Gly Val Phe  
 705 710 715 720

Glu Lys Leu Asp Glu Tyr Ile Tyr Arg His Phe Phe Gly His Thr Phe  
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Ser Pro Pro Tyr Gly Pro Arg Ser Val Tyr Ile Lys Pro Cys His Tyr  
 740 745 750

Ser Ser Leu  
 755

<210> 36  
 <211> 558  
 <212> DNA  
 <213> Homo sapiens

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 <222> (1)..(558)  
 <223> n = g, a, c or t

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<210> 37  
 <211> 86  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MOD\_RES  
 <222> (1)..(86)  
 <223> Xaa = any amino acid

<400> 37  
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 Ala Lys Leu Ile Asp Phe Gly Ser Gly Ala Leu Leu His Asp Glu Pro  
 35 40 45  
 Tyr Thr Asp Phe Asp Gly Thr Arg Val Tyr Ser Pro Pro Glu Trp Ile  
 50 55 60

Ser Arg His Gln Tyr His Ala Leu Pro Ala Thr Val Trp Ser Leu Gly  
65 70 75 80

Ile Xaa Leu Tyr Asp Met  
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<210> 38

<211> 584

<212> DNA

<213> Homo sapiens

<220>

<221> modified\_base

<222> (1)..(584)

<223> n = g, a, c or t

<400> 38

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<210> 39

<211> 2052

<212> DNA

<213> Homo sapiens

<400> 39

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taatagaatc ag 2052

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<210> 40  
 <211> 311  
 <212> PRT  
 <213> Homo sapiens

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      20              25              30

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      35              40              45

Gly His Arg Leu Thr Asp Arg Leu Gln Val Ala Ile Lys Val Ile Pro
      50              55              60

Arg Asn Arg Val Leu Gly Trp Ser Pro Leu Ser Asp Ser Val Thr Cys
      65              70              75              80

Pro Leu Glu Val Ala Leu Leu Trp Lys Val Gly Ala Gly Gly Gly His
      85              90              95

Pro Gly Val Ile Arg Leu Leu Asp Trp Phe Glu Thr Gln Glu Gly Phe
      100             105             110

Met Leu Val Leu Glu Arg Pro Leu Pro Ala Gln Asp Leu Phe Asp Tyr
      115             120             125

Ile Thr Glu Lys Gly Pro Leu Gly Glu Gly Pro Ser Arg Cys Phe Phe
      130             135             140

Gly Gln Val Val Ala Ala Ile Gln His Cys His Ser Arg Gly Val Val
      145             150             155             160

His Arg Asp Ile Lys Asp Glu Asn Ile Leu Ile Asp Leu Arg Arg Gly
      165             170             175

Cys Ala Lys Leu Ile Asp Phe Gly Ser Gly Ala Leu Leu His Asp Glu
      180             185             190

Pro Tyr Thr Asp Phe Asp Gly Thr Arg Val Tyr Ser Pro Pro Glu Trp
      195             200             205

Ile Ser Arg His Gln Tyr His Ala Leu Pro Ala Thr Val Trp Ser Leu
      210             215             220

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Gly Ile Leu Leu Tyr Asp Met Val Cys Gly Asp Ile Pro Phe Glu Arg  
 225 230 235 240  
 Asp Gln Glu Ile Leu Glu Ala Glu Leu His Phe Pro Ala His Val Ser  
 245 250 255  
 Pro Asp Cys Cys Ala Leu Ile Arg Arg Cys Leu Ala Pro Lys Pro Ser  
 260 265 270  
 Ser Arg Pro Ser Leu Glu Glu Ile Leu Leu Asp Pro Trp Met Gln Thr  
 275 280 285  
 Pro Ala Glu Asp Val Pro Leu Asn Pro Ser Lys Gly Gly Pro Ala Pro  
 290 295 300  
 Leu Ala Trp Ser Leu Leu Pro  
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<210> 41  
 <211> 105  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1)..(105)  
 <223> n = g, a, c or t

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<210> 42  
 <211> 1125  
 <212> DNA  
 <213> Homo sapiens

<400> 42  
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 aacaacctta tttccatagt gggcatttgc ctgggcgtcg gcctactcga gctcgggttc 840  
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<210> 43  
 <211> 281  
 <212> PRT  
 <213> Homo sapiens

<400> 43

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	50					55					60				
Gly	Ile	Phe	Thr	Met	Gly	Ile	Ala	Leu	Leu	Gly	Cys	Val	Gly	Ala	Leu
	65				70					75					80
Lys	Glu	Leu	Arg	Cys	Leu	Leu	Gly	Leu	Tyr	Phe	Gly	Met	Leu	Leu	Leu
			85						90					95	
Leu	Phe	Ala	Thr	Gln	Ile	Thr	Leu	Gly	Ile	Leu	Ile	Ser	Thr	Gln	Arg
		100						105					110		
Ala	Gln	Leu	Glu	Arg	Ser	Leu	Arg	Asp	Val	Val	Glu	Lys	Thr	Ile	Gln
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Lys	Tyr	Gly	Thr	Asn	Pro	Glu	Glu	Thr	Ala	Ala	Glu	Glu	Ser	Trp	Asp
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Tyr	Val	Gln	Phe	Gln	Leu	Arg	Cys	Cys	Gly	Trp	His	Tyr	Pro	Gln	Asp
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Trp	Phe	Gln	Val	Leu	Ile	Leu	Arg	Gly	Asn	Gly	Ser	Glu	Ala	His	Arg
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Val	Pro	Cys	Ser	Cys	Tyr	Asn	Leu	Ser	Ala	Thr	Asn	Asp	Ser	Thr	Ile
		180						185					190		
Leu	Asp	Lys	Val	Ile	Leu	Pro	Gln	Leu	Ser	Arg	Leu	Gly	His	Leu	Ala
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Arg	Ser	Arg	His	Ser	Ala	Asp	Ile	Cys	Ala	Val	Pro	Ala	Glu	Ser	His
	210					215					220				
Ile	Tyr	Arg	Glu	Gly	Cys	Ala	Gln	Gly	Leu	Gln	Lys	Trp	Leu	His	Asn
	225				230				235						240
Asn	Leu	Ile	Ser	Ile	Val	Gly	Ile	Cys	Leu	Gly	Val	Gly	Leu	Leu	Glu
			245						250				255		
Leu	Gly	Phe	Met	Thr	Leu	Ser	Ile	Phe	Leu	Cys	Arg	Asn	Leu	Asp	His
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Val	Tyr	Asn	Arg	Leu	Ala	Arg	Tyr	Arg							
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<210> 44  
 <211> 2915  
 <212> DNA  
 <213> Homo sapiens

<400> 44  
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<210> 45  
 <211> 432  
 <212> PRT  
 <213> Homo sapiens

<400> 45

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Arg	Trp	Gly	Ala	Arg	Ala	Gln	Glu	Ala	Ala	Ala	Ala	Ala	Ala	Asp	Gly	35	40	45	
Pro	Pro	Ala	Ala	Asp	Gly	Glu	Asp	Gly	Gln	Asp	Pro	His	Ser	Lys	His	50	55	60	
Leu	Tyr	Thr	Ala	Asp	Met	Phe	Thr	His	Gly	Ile	Gln	Ser	Ala	Ala	His	65	70	75	80
Phe	Val	Met	Phe	Phe	Ala	Pro	Trp	Cys	Gly	His	Cys	Gln	Arg	Leu	Gln	85	90	95	
Pro	Thr	Trp	Asn	Asp	Leu	Gly	Asp	Lys	Tyr	Asn	Ser	Met	Glu	Asp	Ala	100	105	110	
Lys	Val	Tyr	Val	Ala	Lys	Val	Asp	Cys	Thr	Ala	His	Ser	Asp	Val	Cys	115	120	125	
Ser	Ala	Gln	Gly	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Lys	Leu	Phe	Lys	Pro	130	135	140	
Gly	Gln	Glu	Ala	Val	Lys	Tyr	Gln	Gly	Pro	Arg	Asp	Phe	Gln	Thr	Leu	145	150	155	160
Glu	Asn	Trp	Met	Leu	Gln	Thr	Leu	Asn	Glu	Glu	Pro	Val	Thr	Pro	Glu	165	170	175	
Pro	Glu	Val	Glu	Pro	Pro	Ser	Ala	Pro	Glu	Leu	Lys	Gln	Gly	Leu	Tyr	180	185	190	
Glu	Leu	Ser	Ala	Ser	Asn	Phe	Glu	Leu	His	Val	Ala	Gln	Gly	Asp	His	195	200	205	
Phe	Ile	Lys	Phe	Phe	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Ala	Leu	Ala	210	215	220	
Pro	Thr	Trp	Glu	Gln	Leu	Ala	Leu	Gly	Leu	Glu	His	Ser	Glu	Thr	Val	225	230	235	240
Lys	Ile	Gly	Lys	Val	Asp	Cys	Thr	Gln	His	Tyr	Glu	Leu	Cys	Ser	Gly	245	250	255	
Asn	Gln	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Trp	Phe	Arg	Asp	Gly	Lys	260	265	270	
Lys	Val	Asp	Gln	Tyr	Lys	Gly	Lys	Arg	Asp	Leu	Glu	Ser	Leu	Arg	Glu	275	280	285	
Tyr	Val	Glu	Ser	Gln	Leu	Gln	Arg	Thr	Glu	Thr	Gly	Ala	Thr	Glu	Thr	290	295	300	
Val	Thr	Pro	Ser	Glu	Ala	Pro	Val	Leu	Ala	Ala	Glu	Pro	Glu	Ala	Asp	305	310	315	320

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 Cys Arg Thr Leu Ala Pro Thr Trp Glu Glu Leu Ser Lys Lys Glu Phe  
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 Pro Gly Leu Ala Gly Val Lys Ile Ala Glu Val Asp Cys Thr Ala Glu  
 370 375 380  
 Arg Asn Ile Cys Ser Lys Tyr Ser Val Arg Gly Tyr Pro Thr Leu Leu  
 385 390 395 400  
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<210> 46  
 <211> 551  
 <212> DNA  
 <213> Homo sapiens

<400> 46  
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 <211> 3252  
 <212> DNA  
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<210> 48

<211> 762

<212> PRT

<213> Homo sapiens

<400> 48

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Gly Gly Gly Gln Gly Pro Met Pro Arg Val Arg Tyr Tyr Ala Gly Asp  
35 40 45

Glu Arg Arg Ala Leu Ser Phe Phe His Gln Lys Gly Leu Gln Asp Phe  
50 55 60

Asp Thr Leu Leu Leu Ser Gly Asp Gly Asn Thr Leu Tyr Val Gly Ala  
 65 70 75 80  
 Arg Glu Ala Ile Leu Ala Leu Asp Ile Gln Asp Pro Gly Val Pro Arg  
 85 90 95  
 Leu Lys Asn Met Ile Pro Trp Pro Ala Ser Asp Arg Lys Lys Ser Glu  
 100 105 110  
 Cys Ala Phe Lys Lys Lys Ser Asn Glu Thr Gln Cys Phe Asn Phe Ile  
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 130 135 140  
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 Pro Phe Asp Pro Ala His Lys His Thr Ala Val Leu Val Asp Gly Met  
 180 185 190  
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 195 200 205  
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 225 230 235 240  
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 Phe Glu Arg Leu His Thr Ser Arg Val Ala Arg Val Cys Lys Asn Asp  
 260 265 270  
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 325 330 335  
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 340 345 350  
 Gly Lys Phe Lys Glu Leu Asn Lys Glu Thr Ser Arg Trp Thr Thr Tyr  
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 Arg Gly Pro Glu Thr Asn Pro Arg Pro Gly Ser Cys Ser Val Gly Pro  
 370 375 380

Ser Ser Asp Lys Ala Leu Thr Phe Met Lys Asp His Phe Leu Met Asp  
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 405 410 415  
 Thr Arg Leu Ala Val Glu Thr Ala Gln Gly Leu Asp Gly His Ser His  
 420 425 430  
 Leu Val Met Tyr Leu Gly Thr Thr Thr Gly Ser Leu His Lys Ala Val  
 435 440 445  
 Val Ser Gly Asp Ser Ser Ala His Leu Val Glu Glu Ile Gln Leu Phe  
 450 455 460  
 Pro Asp Pro Glu Pro Val Arg Asn Leu Gln Leu Ala Pro Thr Gln Gly  
 465 470 475 480  
 Ala Val Phe Val Gly Phe Ser Gly Gly Val Trp Arg Val Pro Arg Ala  
 485 490 495  
 Asn Cys Ser Val Tyr Glu Ser Cys Val Asp Cys Val Leu Ala Arg Asp  
 500 505 510  
 Pro His Cys Ala Trp Asp Pro Glu Ser Arg Thr Cys Cys Leu Leu Ser  
 515 520 525  
 Ala Pro Asn Leu Asn Ser Trp Lys Gln Asp Met Glu Arg Gly Asn Pro  
 530 535 540  
 Glu Trp Ala Cys Ala Ser Gly Pro Met Ser Arg Ser Leu Arg Pro Gln  
 545 550 555 560  
 Ser Arg Pro Gln Ile Ile Lys Glu Val Leu Ala Val Pro Asn Ser Ile  
 565 570 575  
 Leu Glu Leu Pro Cys Pro His Leu Ser Ala Leu Ala Ser Tyr Tyr Trp  
 580 585 590  
 Ser His Gly Pro Ala Ala Val Pro Glu Ala Ser Ser Thr Val Tyr Asn  
 595 600 605  
 Gly Ser Leu Leu Leu Ile Val Gln Asp Gly Val Gly Gly Leu Tyr Gln  
 610 615 620  
 Cys Trp Ala Thr Glu Asn Gly Phe Ser Tyr Pro Val Ile Ser Tyr Trp  
 625 630 635 640  
 Val Asp Ser Gln Asp Gln Thr Leu Ala Leu Asp Pro Glu Leu Ala Gly  
 645 650 655  
 Ile Pro Arg Glu His Val Lys Val Pro Leu Thr Arg Val Ser Gly Gly  
 660 665 670  
 Ala Ala Leu Ala Ala Gln Gln Ser Tyr Trp Pro His Phe Val Thr Val  
 675 680 685  
 Thr Val Leu Phe Ala Leu Val Leu Ser Gly Ala Leu Ile Ile Leu Val  
 690 695 700



Ala Ser Pro Leu Arg Ala Leu Arg Ala Arg Gly Lys Val Gln Gly Cys  
705 710 715 720

Glu Thr Leu Arg Pro Gly Glu Lys Ala Pro Leu Ser Arg Glu Gln His  
725 730 735

Leu Gln Ser Pro Lys Glu Cys Arg Thr Ser Ala Ser Asp Val Asp Ala  
740 745 750

Asp Asn Asn Cys Leu Gly Thr Glu Val Ala  
755 760

<210> 49  
<211> 182  
<212> DNA  
<213> Homo sapiens

<220>  
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<222> (1)..(182)  
<223> n = g, a, c or t

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<213> Homo sapiens

<220>  
<221> MOD\_RES  
<222> (1)..(60)  
<223> Xaa = any amino acid

<400> 50  
Gln Gln Ser Cys Gly Thr Tyr Leu Arg Val Arg Gln Pro Pro Pro Arg  
1 5 10 15

Pro Phe Leu Asp Met Gly Glu Gly Thr Lys Asn Arg Ile Ile Thr Ala  
20 25 30

Glu Gly Ile Ile Leu Leu Phe Cys Ala Val Val Pro Gly Thr Leu Leu  
35 40 45

Leu Xaa Arg Lys Arg Trp Gln Glu Arg Xaa Leu Xaa  
50 55 60

<210> 51  
<211> 182  
<212> DNA  
<213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1)..(182)  
 <223> n = g, a, c or t

<400> 51  
 accagcagtc ctgcggcacc tacctccgcg tgcgccagcc gccccccagg cccttcctgg 60  
 acatggggga gggcaccaag aaccgaatca tcacagccga ggggatcatc ctctgttct 120  
 gcgcggtggt gcctgggacg ctgctgctgt tnaggaaacg atggcaagaa cganaactcn 180  
 gg 182

<210> 52  
 <211> 60  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> MOD\_RES  
 <222> (1)..(60)  
 <223> Xaa = any amino acid

<400> 52  
 Gln Gln Ser Cys Gly Thr Tyr Leu Arg Val Arg Gln Pro Pro Pro Arg  
 1 5 10 15  
 Pro Phe Leu Asp Met Gly Glu Gly Thr Lys Asn Arg Ile Ile Thr Ala  
 20 25 30  
 Glu Gly Ile Ile Leu Leu Phe Cys Ala Val Val Pro Gly Thr Leu Leu  
 35 40 45  
 Leu Xaa Arg Lys Arg Trp Gln Glu Arg Xaa Leu Xaa  
 50 55 60

<210> 53  
 <211> 1107  
 <212> DNA  
 <213> Homo sapiens

<400> 53  
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 caagctctgc ctgccaccat cttcctcctc ttctgtctgt ctgctgtcta cctgggccct 120  
 ggggtgccagg cctgtggat gcacaaggtc ccagcatcat tgatggtgag cctgggggaa 180  
 gacgccact tccaatgccc gcacaatagc agcaacaacg ccaacgtcac ctgggtggcg 240  
 gtctccatg gcaactacac gtggccccct gagttcttgg gcccgggcga ggacccaat 300  
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 caggagggca acgagtcata ccagcagtc tgcggcacct acctccgct gcgccagccg 420  
 cccccaggc cttccttggga catgggggag ggcaccaaga accgaatcat cacagccgag 480  
 gggatcatcc tctgtttctg gcgcggtggtg cctgggacgc tgctgctgtt caggaaaacga 540  
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 gtgtcccaact cttcttccct ctaaactgcc ccacctcta acctaatccc cagccccgc 960  
 tgcctttccc aggtccccc caccagcgg gtaatgagcc cttaatcgct gcctctaggg 1020  
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 tagtgataat aaattcttcc caactgc 1107

<210> 54  
 <211> 226  
 <212> PRT  
 <213> Homo sapiens

<400> 54  
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                   20                          25                          30  
 Leu Trp Met His Lys Val Pro Ala Ser Leu Met Val Ser Leu Gly Glu  
           35                          40                          45  
 Asp Ala His Phe Gln Cys Pro His Asn Ser Ser Asn Asn Ala Asn Val  
           50                          55                          60  
 Thr Trp Trp Arg Val Leu His Gly Asn Tyr Thr Trp Pro Pro Glu Phe  
           65                          70                          75                          80  
 Leu Gly Pro Gly Glu Asp Pro Asn Gly Thr Leu Ile Ile Gln Asn Val  
                   85                          90                          95  
 Asn Lys Ser His Gly Gly Ile Tyr Val Cys Arg Val Gln Glu Gly Asn  
                   100                          105                          110  
 Glu Ser Tyr Gln Gln Ser Cys Gly Thr Tyr Leu Arg Val Arg Gln Pro  
           115                          120                          125  
 Pro Pro Arg Pro Phe Leu Asp Met Gly Glu Gly Thr Lys Asn Arg Ile  
           130                          135                          140  
 Ile Thr Ala Glu Gly Ile Ile Leu Leu Phe Cys Ala Val Val Pro Gly  
           145                          150                          155                          160  
 Thr Leu Leu Leu Phe Arg Lys Arg Trp Gln Asn Glu Lys Leu Gly Leu  
                   165                          170                          175  
 Asp Ala Gly Asp Glu Tyr Glu Asp Glu Asn Leu Tyr Glu Gly Leu Asn  
                   180                          185                          190  
 Leu Asp Asp Cys Ser Met Tyr Glu Asp Ile Ser Arg Gly Leu Gln Gly  
           195                          200                          205  
 Thr Tyr Gln Asp Val Gly Ser Leu Asn Ile Gly Asp Val Gln Leu Glu  
           210                          215                          220  
 Lys Pro  
 225

<210> 55  
 <211> 1038  
 <212> DNA  
 <213> Homo sapiens

<400> 55  
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 ccatggggca tcattctgga gtccctggcc atacttgga tcgtgggcac aattctgcta 120  
 ctcttagcat ttctcttct catgcgaaag atccaagact gcagccagtg gaatgtcctc 180

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cccaccagc tcctcttctt cctgagtgtc ctggggctct tcggactcgc ttttgccttc 240
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gctctctgtt tctcatgcct cttagctcat gcctccaatc tagtgaagct gggtcgggg 360
tgtgtctctt tctcctggac gacaattctg tgcattgcta ttgggtgcag tctgttgcaa 420
atcattattg cactgagta tgtgactctc atcatgacca gaggtatgat gtttgtgaat 480
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gacagtgatg gagctgagga ggatgtagca ttaacttcat atggtactcc cattcagccg 960
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<210> 56  
 <211> 345  
 <212> PRT  
 <213> Homo sapiens

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<400> 56
Met Tyr Lys Asp Cys Ile Glu Ser Thr Gly Asp Tyr Phe Leu Leu Cys
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Asp Ala Glu Gly Pro Trp Gly Ile Ile Leu Glu Ser Leu Ala Ile Leu
      20             25             30

Gly Ile Val Val Thr Ile Leu Leu Leu Leu Ala Phe Leu Phe Leu Met
      35             40             45

Arg Lys Ile Gln Asp Cys Ser Gln Trp Asn Val Leu Pro Thr Gln Leu
      50             55             60

Leu Phe Leu Leu Ser Val Leu Gly Leu Phe Gly Leu Ala Phe Ala Phe
      65             70             75             80

Ile Ile Glu Leu Asn Gln Gln Thr Ala Pro Val Arg Tyr Phe Leu Phe
      85             90             95

Gly Val Leu Phe Ala Leu Cys Phe Ser Cys Leu Leu Ala His Ala Ser
      100            105            110

Asn Leu Val Lys Leu Val Arg Gly Cys Val Ser Phe Ser Trp Thr Thr
      115            120            125

Ile Leu Cys Ile Ala Ile Gly Cys Ser Leu Leu Gln Ile Ile Ile Ala
      130            135            140

Thr Glu Tyr Val Thr Leu Ile Met Thr Arg Gly Met Met Phe Val Asn
      145            150            155            160

Met Thr Pro Cys Gln Leu Asn Val Asp Phe Val Val Leu Leu Val Tyr
      165            170            175

Val Leu Phe Leu Met Ala Leu Thr Phe Phe Val Ser Lys Ala Thr Phe
      180            185            190

Cys Gly Pro Cys Glu Asn Trp Lys Gln His Gly Arg Leu Ile Phe Ile
      195            200            205

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Thr Val Leu Phe Ser Ile Ile Ile Trp Val Val Trp Ile Ser Met Leu  
 210 215 220  
 Leu Arg Gly Asn Pro Gln Phe Gln Arg Gln Pro Gln Trp Asp Asp Pro  
 225 230 235 240  
 Val Val Cys Ile Ala Leu Val Thr Asn Ala Trp Val Phe Leu Leu Leu  
 245 250 255  
 Tyr Ile Val Pro Glu Leu Cys Ile Leu Tyr Arg Ser Cys Arg Gln Glu  
 260 265 270  
 Cys Pro Leu Gln Gly Asn Ala Cys Pro Val Thr Ala Tyr Gln His Ser  
 275 280 285  
 Phe Gln Val Glu Asn Gln Glu Leu Ser Arg Ala Arg Asp Ser Asp Gly  
 290 295 300  
 Ala Glu Glu Asp Val Ala Leu Thr Ser Tyr Gly Thr Pro Ile Gln Pro  
 305 310 315 320  
 Gln Thr Val Asp Pro Thr Gln Glu Cys Phe Ile Pro Gln Ala Lys Leu  
 325 330 335  
 Ser Pro Gln Gln Asp Ala Gly Gly Val  
 340 345

<210> 57  
 <211> 2457  
 <212> DNA  
 <213> Homo sapiens

<400> 57  
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 ctgcagccct cgcctgggag agcggcgcg cgggcaggcg cccaagagag catcgagcag 180  
 cggaaccgc gaagccggcc cgcagccgcg acccgcgag cctgccgctc tcccgcgcgc 240  
 ggtccgggca gcatgaggcg cgcggcgctc tggtctctggc tgtgcgcgct ggcgctgagc 300  
 ctgcagccgg ccctgccgca aattgtggct actaatttgc cccctgaaga tcaagatggc 360  
 tctggggatg actctgacaa cttctccggc tcaggtgcag gtgctttgca agatatcacc 420  
 ttgtcacagc agacccctc cacttggaag gacacgcagc tcctgacggc tattcccacg 480  
 tctccagaac ccaccggcct ggaggctaca gctgcctcca cctccaccct gccggctgga 540  
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 cgggagcagg aggccacccc ccgaccagg gagaccacac agctcccag cactcatcag 660  
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<210> 58

<211> 310

<212> PRT

<213> Homo sapiens

<400> 58

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Met Arg Arg Ala Ala Leu Trp Leu Trp Leu Cys Ala Leu Ala Leu Ser
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Leu Gln Pro Ala Leu Pro Gln Ile Val Ala Thr Asn Leu Pro Pro Glu
              20              25              30

Asp Gln Asp Gly Ser Gly Asp Asp Ser Asp Asn Phe Ser Gly Ser Gly
              35              40              45

Ala Gly Ala Leu Gln Asp Ile Thr Leu Ser Gln Gln Thr Pro Ser Thr
              50              55              60

Trp Lys Asp Thr Gln Leu Leu Thr Ala Ile Pro Thr Ser Pro Glu Pro
  65              70              75              80

Thr Gly Leu Glu Ala Thr Ala Ala Ser Thr Ser Thr Leu Pro Ala Gly
              85              90              95

Glu Gly Pro Lys Glu Gly Glu Ala Val Val Leu Pro Glu Val Glu Pro
              100              105              110

Gly Leu Thr Ala Arg Glu Gln Glu Ala Thr Pro Arg Pro Arg Glu Thr
              115              120              125

Thr Gln Leu Pro Thr Thr His Gln Ala Ser Thr Thr Thr Ala Thr Thr
              130              135              140

Ala Gln Glu Pro Ala Thr Ser His Pro His Arg Asp Met Gln Pro Gly
  145              150              155              160

His His Glu Thr Ser Thr Pro Ala Gly Pro Ser Gln Ala Asp Leu His
              165              170              175

Thr Pro His Thr Glu Asp Gly Gly Pro Ser Ala Thr Glu Arg Ala Ala
              180              185              190

Glu Asp Gly Ala Ser Ser Gln Leu Pro Ala Ala Glu Gly Ser Gly Glu
  195              200              205

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Gln Asp Phe Thr Phe Glu Thr Ser Gly Glu Asn Thr Ala Val Val Ala  
 210 215 220  
 Val Glu Pro Asp Arg Arg Asn Gln Ser Pro Val Asp Gln Gly Ala Thr  
 225 230 235 240  
 Gly Ala Ser Gln Gly Leu Leu Asp Arg Lys Glu Val Leu Gly Gly Val  
 245 250 255  
 Ile Ala Val Gly Leu Val Gly Leu Ile Phe Ala Val Cys Leu Val Gly  
 260 265 270  
 Phe Met Leu Tyr Arg Met Lys Lys Lys Asp Glu Gly Ser Tyr Ser Leu  
 275 280 285  
 Glu Glu Pro Lys Gln Ala Asn Gly Gly Ala Tyr Gln Lys Pro Thr Lys  
 290 295 300  
 Gln Glu Glu Phe Tyr Ala  
 305 310

<210> 59  
 <211> 357  
 <212> DNA  
 <213> Homo sapiens

<400> 59  
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 ctctagagg gggttccaat gaggcaggct gctgtcacct cgacctcctt gaccatcaag 240  
 tctgtcttca cccggagcga gctcaagttc tccccacagt ggagtcacca tgggaagatt 300  
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<210> 60  
 <211> 3260  
 <212> DNA  
 <213> Homo sapiens

<400> 60  
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cacttcaaag aaaaaaaaaa 3260

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<210> 61

<211> 847

<212> PRT

<213> Homo sapiens

<400> 61

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Met His Leu Leu Gly Pro Trp Leu Leu Leu Leu Val Leu Glu Tyr Leu
  1             5             10             15

Ala Phe Ser Asp Ser Ser Lys Trp Val Phe Glu His Pro Glu Thr Leu
  20             25             30

Tyr Ala Trp Glu Gly Ala Cys Val Trp Ile Pro Cys Thr Tyr Arg Ala
  35             40             45

Leu Asp Gly Asp Leu Glu Ser Phe Ile Leu Phe His Asn Pro Glu Tyr
  50             55             60

Asn Lys Asn Thr Ser Lys Phe Asp Gly Thr Arg Leu Tyr Glu Ser Thr
  65             70             75             80

Lys Asp Gly Lys Val Pro Ser Glu Gln Lys Arg Val Gln Phe Leu Gly
  85             90             95

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Asp Lys Asn Lys Asn Cys Thr Leu Ser Ile His Pro Val His Leu Asn  
 100 105 110  
 Asp Ser Gly Gln Leu Gly Leu Arg Met Glu Ser Lys Thr Glu Lys Trp  
 115 120 125  
 Met Glu Arg Ile His Leu Asn Val Ser Glu Arg Pro Phe Pro Pro His  
 130 135 140  
 Ile Gln Leu Pro Pro Glu Ile Gln Glu Ser Gln Glu Val Thr Leu Thr  
 145 150 155 160  
 Cys Leu Leu Asn Phe Ser Cys Tyr Gly Tyr Pro Ile Gln Leu Gln Trp  
 165 170 175  
 Leu Leu Glu Gly Val Pro Met Arg Gln Ala Ala Val Thr Ser Thr Ser  
 180 185 190  
 Leu Thr Ile Lys Ser Val Phe Thr Arg Ser Glu Leu Lys Phe Ser Pro  
 195 200 205  
 Gln Trp Ser His His Gly Lys Ile Val Thr Cys Gln Leu Gln Asp Ala  
 210 215 220  
 Asp Gly Lys Phe Leu Ser Asn Asp Thr Val Gln Leu Asn Val Lys His  
 225 230 235 240  
 Thr Pro Lys Leu Glu Ile Lys Val Thr Pro Ser Asp Ala Ile Val Arg  
 245 250 255  
 Glu Gly Asp Ser Val Thr Met Thr Cys Glu Val Ser Ser Ser Asn Pro  
 260 265 270  
 Glu Tyr Thr Thr Val Ser Trp Leu Lys Asp Gly Thr Ser Leu Lys Lys  
 275 280 285  
 Gln Asn Thr Phe Thr Leu Asn Leu Arg Glu Val Thr Lys Asp Gln Ser  
 290 295 300  
 Gly Lys Tyr Cys Cys Gln Val Ser Asn Asp Val Gly Pro Gly Arg Ser  
 305 310 315 320  
 Glu Glu Val Phe Leu Gln Val Gln Tyr Ala Pro Glu Pro Ser Thr Val  
 325 330 335  
 Gln Ile Leu His Ser Pro Ala Val Glu Gly Ser Gln Val Glu Phe Leu  
 340 345 350  
 Cys Met Ser Leu Ala Asn Pro Leu Pro Thr Asn Tyr Thr Trp Tyr His  
 355 360 365  
 Asn Gly Lys Glu Met Gln Gly Arg Thr Glu Glu Lys Val His Ile Pro  
 370 375 380  
 Lys Ile Leu Pro Trp His Ala Gly Thr Tyr Ser Cys Val Ala Glu Asn  
 385 390 395 400  
 Ile Leu Gly Thr Gly Gln Arg Gly Pro Gly Ala Glu Leu Asp Val Gln  
 405 410 415

Tyr Pro Pro Lys Lys Val Thr Thr Val Ile Gln Asn Pro Met Pro Ile  
420 425 430  
Arg Glu Gly Asp Thr Val Thr Leu Ser Cys Asn Tyr Asn Ser Ser Asn  
435 440 445  
Pro Ser Val Thr Arg Tyr Glu Trp Lys Pro His Gly Ala Trp Glu Glu  
450 455 460  
Pro Ser Leu Gly Val Leu Lys Ile Gln Asn Val Gly Trp Asp Asn Thr  
465 470 475 480  
Thr Ile Ala Cys Ala Arg Cys Asn Ser Trp Cys Ser Trp Ala Ser Pro  
485 490 495  
Val Ala Leu Asn Val Gln Tyr Ala Pro Arg Asp Val Arg Val Arg Lys  
500 505 510  
Ile Lys Pro Leu Ser Glu Ile His Ser Gly Asn Ser Val Ser Leu Gln  
515 520 525  
Cys Asp Phe Ser Ser Ser His Pro Lys Glu Val Gln Phe Phe Trp Glu  
530 535 540  
Lys Asn Gly Arg Leu Leu Gly Lys Glu Ser Gln Leu Asn Phe Asp Ser  
545 550 555 560  
Ile Ser Pro Glu Asp Ala Gly Ser Tyr Ser Cys Trp Val Asn Asn Ser  
565 570 575  
Ile Gly Gln Thr Ala Ser Lys Ala Trp Thr Leu Glu Val Leu Tyr Ala  
580 585 590  
Pro Arg Arg Leu Arg Val Ser Met Ser Pro Gly Asp Gln Val Met Glu  
595 600 605  
Gly Lys Ser Ala Thr Leu Thr Cys Glu Ser Asp Ala Asn Pro Pro Val  
610 615 620  
Ser His Tyr Thr Trp Phe Asp Trp Asn Asn Gln Ser Leu Pro His His  
625 630 635 640  
Ser Gln Lys Leu Arg Leu Glu Pro Val Lys Val Gln His Ser Gly Ala  
645 650 655  
Tyr Trp Cys Gln Gly Thr Asn Ser Val Gly Lys Gly Arg Ser Pro Leu  
660 665 670  
Ser Thr Leu Thr Val Tyr Tyr Ser Pro Glu Thr Ile Gly Arg Arg Val  
675 680 685  
Ala Val Gly Leu Gly Ser Cys Leu Ala Ile Leu Ile Leu Ala Ile Cys  
690 695 700  
Gly Leu Lys Leu Gln Arg Arg Trp Lys Arg Thr Gln Ser Gln Gln Gly  
705 710 715 720  
Leu Gln Glu Asn Ser Ser Gly Gln Ser Phe Phe Val Arg Asn Lys Lys  
725 730 735

Val Arg Arg Ala Pro Leu Ser Glu Gly Pro His Ser Leu Gly Cys Tyr  
740 745 750

Asn Pro Met Met Glu Asp Gly Ile Ser Tyr Thr Thr Leu Arg Phe Pro  
755 760 765

Glu Met Asn Ile Pro Arg Thr Gly Asp Ala Glu Ser Ser Glu Met Gln  
770 775 780

Arg Pro Pro Arg Thr Cys Asp Asp Thr Val Thr Tyr Ser Ala Leu His  
785 790 795 800

Lys Arg Gln Val Gly Asp Tyr Glu Asn Val Ile Pro Asp Phe Pro Glu  
805 810 815

Asp Glu Gly Ile His Tyr Ser Glu Leu Ile Gln Phe Gly Val Gly Glu  
820 825 830

Arg Pro Gln Ala Gln Glu Asn Val Asp Tyr Val Ile Leu Lys His  
835 840 845

<210> 62  
<211> 340  
<212> DNA  
<213> Homo sapiens

<400> 62  
ctgggggggtc cgggaaaggg gttggggccat gagccaggca gctccgaagc agtcactgag 60  
gccaggggagc ctgcacccag gtcattggggc gacctggctc tcaactcctgg cctgggtgct 120  
cacctacaga ccacttcaact tcccctgtcc gcagcgtcac tatgtcctca taggtggctg 180  
tctggtcaat gtccaggccc tcgtaggtgt gatcttcctc catgccagcc ttgctgtcat 240  
ccttggtccag cagcaggaag ataggcacga tgatgaagag gatgatcagc agcgtctgga 300  
tcatgatgat accatccttc agcgtgttcc tctgcttcag 340

<210> 63  
<211> 79  
<212> PRT  
<213> Homo sapiens

<400> 63  
Leu Lys Gln Arg Asn Thr Leu Lys Asp Gly Ile Ile Met Ile Gln Thr  
1 5 10 15

Leu Leu Ile Ile Leu Phe Ile Ile Val Pro Ile Phe Leu Leu Leu Asp  
20 25 30

Lys Asp Asp Ser Lys Ala Gly Met Glu Glu Asp His Thr Tyr Glu Gly  
35 40 45

Leu Asp Ile Asp Gln Thr Ala Thr Tyr Glu Asp Ile Val Thr Leu Arg  
50 55 60

Thr Gly Glu Val Lys Trp Ser Val Gly Glu His Pro Gly Gln Glu  
65 70 75

<210> 64  
 <211> 340  
 <212> DNA  
 <213> Homo sapiens

<400> 64  
 ctgggggggtc cgggaaagg gttggggccat gagccaggca gctccgaagc agtcactgag 60  
 gccagggagc ctgcacccag gtcattggggc gacctggctc tcaactcctgg cctgggtgct 120  
 cacctacaga ccactttact tcccctgtcc gcagcgtcac tatgtcctca taggtggctg 180  
 tctgggtcaat gtccaggccc tcgtagggtg gatcttctc catgccagcc ttgctgtcat 240  
 ccttgctccag cagcaggaag ataggcacga tgatgaagag gatgatcagc agcgtctgga 300  
 tcatgatgat accatccttc agcgtgttcc tctgcttcag 340

<210> 65  
 <211> 1226  
 <212> DNA  
 <213> Homo sapiens

<400> 65  
 ccacgcgtcc gccacgcgt ccgcagagcg gtgaccatgg ccaggctggc gttgtctcct 60  
 gtgcccagcc actggatggg ggcgttgctg ctgctgctct cagctgagcc agtaccagca 120  
 gccagatcgg aggaaccggt cccgaatccc aaaggtagtg cttgttcgcg gatctggcag 180  
 agcccacgtt tcatagccag gaaacggggc ttcacggtga aaatgcactg ctacatgaac 240  
 agcgcctccg gcaatgtgag ctggctctgg aagcaggaga tggacgagaa tccccagcag 300  
 ctgaagctgg aaaagggccg catggaagag tcccagaacg aatctctcgc caccctcacc 360  
 atccaaggca tccggtttga ggacaatggc atctacttct gccagcagaa gtgcaacaac 420  
 acctcggagg tctaccaggg ctgcggcaca gagctgagcgc tcatgggatt cagcaccttg 480  
 gcacagctga agcagaggaa cacgctgaag gatggatatca tcatgatcca gacgctgctg 540  
 atcatcctct tcatcatcgt gcctatcttc ctgctgctgg acaaggatga cagcaaggct 600  
 ggcattggagg aagatcacac ctacgagggc ctggacattg accagacagc cacctatgag 660  
 gacatagtga cgctgcggac aggggaagtg aagtgggtctg taggtgagca cccaggccag 720  
 gagtgagagc caggctcggcc catgacctgg gtgcaggctc cctggcctca gtgactgctt 780  
 cggagctgcc tggtcatgag cccaaccctt tcccgggacc cccagctgg cctctgaagc 840  
 tggcccacca gagctgccat ttgtctccag cccctgggtc ccagctcttg ccaaagggcc 900  
 tggagtagaa ggacaacagg gcagcaactt ggaggaggtt ctctggggat ggacgggacc 960  
 cagccttctg ggggtgctat gaggtgatcc gtccccacac atggggatggg ggaggcagag 1020  
 actggtccag agcccgcaaa tggactcgga gccgagggcc tcccagcaga gcttgggaag 1080  
 ggccatggac ccaactgggc cccagaagag ccacaggaac atcattctc tcccgaacc 1140  
 actccacccc cagggaggcc ctggcctcca gtgccttccc ccgtggaata aacggtgtgt 1200  
 cctgagaaac caaaaaaaaa aaaaaa 1226

<210> 66  
 <211> 229  
 <212> PRT  
 <213> Homo sapiens

<400> 66  
 Met Ala Arg Leu Ala Leu Ser Pro Val Pro Ser His Trp Met Val Ala  
 1 5 10 15  
 Leu Leu Leu Leu Leu Ser Ala Glu Pro Val Pro Ala Ala Arg Ser Glu  
 20 25 30  
 Asp Arg Tyr Arg Asn Pro Lys Gly Ser Ala Cys Ser Arg Ile Trp Gln  
 35 40 45  
 Ser Pro Arg Phe Ile Ala Arg Lys Arg Gly Phe Thr Val Lys Met His  
 50 55 60

Cys Tyr Met Asn Ser Ala Ser Gly Asn Val Ser Trp Leu Trp Lys Gln  
 65 70 75 80  
 Glu Met Asp Glu Asn Pro Gln Gln Leu Lys Leu Glu Lys Gly Arg Met  
 85 90 95  
 Glu Glu Ser Gln Asn Glu Ser Leu Ala Thr Leu Thr Ile Gln Gly Ile  
 100 105 110  
 Arg Phe Glu Asp Asn Gly Ile Tyr Phe Cys Gln Gln Lys Cys Asn Asn  
 115 120 125  
 Thr Ser Glu Val Tyr Gln Gly Cys Gly Thr Glu Leu Arg Val Met Gly  
 130 135 140  
 Phe Ser Thr Leu Ala Gln Leu Lys Gln Arg Asn Thr Leu Lys Asp Gly  
 145 150 155 160  
 Ile Ile Met Ile Gln Thr Leu Leu Ile Ile Leu Phe Ile Ile Val Pro  
 165 170 175  
 Ile Phe Leu Leu Leu Asp Lys Asp Asp Ser Lys Ala Gly Met Glu Glu  
 180 185 190  
 Asp His Thr Tyr Glu Gly Leu Asp Ile Asp Gln Thr Ala Thr Tyr Glu  
 195 200 205  
 Asp Ile Val Thr Leu Arg Thr Gly Glu Val Lys Trp Ser Val Gly Glu  
 210 215 220  
 His Pro Gly Gln Glu  
 225

<210> 67  
 <211> 449  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (16)  
 <223> n = g, a, c or t

<400> 67  
 aaaattgatc acaacnaggg aaaacaaaat aaaattaggg ggcaaagggt aggagtatgg 60  
 ggggagggga gagcaaacct atcgaatata tcttagaatt ttgctcagaa atcactgctg 120  
 cctctcaagt gttgcattgt cctgcctaa accaagaagg ctaaacaag cccctcctgt 180  
 ttgaattctt aaggttaagaa atttctaagc taagaaaaca ctattgccta aaaccaatga 240  
 tagtggagct catttacaaa taggcattgcc tcacacacac agtccaaagg caagacactg 300  
 gctttgaaat taggctcatg atgtgattcc tattatatgt acctgatttt tttaggcccc 360  
 aggtatgtgg accagagtta atgtcatgac tcttcaaaga tatgatgaaa agttgcccta 420  
 gaaatctaga gatgcatgtt tattaatt 449

<210> 68  
 <211> 2359  
 <212> DNA  
 <213> Homo sapiens

<400> 68

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ctttcaagaa aatacatctg tgctgtatct tccccctccc tcaggccatg atctctgctg 60
ttttccttac taactggcat gtcagtacaa gagtgattgt gaagctgctc cggaaggggt 120
ttatgctaac ctctgttgct tgatgacatg tctcaggac tctgatatta aaactcaatc 180
cttagataac aggtagcttt atcatggaag taggtagcaa tttggaatta gaccattctt 240
agttatcttt ttcttaatga attgatacat gcactttaaa aaatatcttt gttatttttg 300
gaagaaaaaac tcagactttt aaaaaagtgt atattgtccc attataatat gtatatggaa 360
gagtgaaatc tgaacgctgt cttatattaa gcagtagaat taggtattat cataaaaaagt 420
cttaatctgt agggaatatg agtttatgtt tatgagtcct gctcagtcct tctttgagag 480
aattagttga aaccagactc ctaaagctg cttttatatt tgtttgtaa gaccatttat 540
ctgcagaagg ttgcctttta accccagtggt ttctaagggtg tggaattgag tgaccctaata 600
atttacataa gagacttggt ttagtggagc ataagggagg ggcataagtt acaccgtttt 660
gtgctgcttg agaactgtct tttaaaattg atcacaacga gggaaaaaaa aataaaaatta 720
ggggggcaag ggtaggagta tggggggagg ggagagcaaa cctatcgaat atatcttaga 780
atcttgctca gaaatcactg ctgcctctca agtggtgcat tgcctctgcc taaaccaaga 840
aggctaaaca aagccccctc tgtttgaatt ctttaaggtaa gaaatttcta agctaagaaa 900
acactattgc ctaaaaccaa tgatagtggg gctcatttac aaataggcat gcctcacaca 960
cacagtccaa aggcaagaca ctggctttga aattaggctc atgatgtgat tcctattata 1020
tgtacctgat ttttttaggc cccaggtatg tggaccagag ttaatgtcat gactcttcaa 1080
agatatgatg aaaagtggcc ctagaatctc agagatgcac gtttatttaa ttccatagtt 1140
taaaaaaaaaa ttttaagcagg tagttgtggc ttatctgggg gcaaaaataat atatgtgaaa 1200
ttgcttccag aggacaaaagt atattttcta aagtcctgaa ataggatcat gaacccttct 1260
gaagtttttg tttgaaatat tatagtatat gatattacca aagagccctt aattcagagt 1320
ttaaggggct ctcttcctga actctcttca tcaactcaggg ttgaatgtgt aatgttcctt 1380
gctattgatt gttattgttg attcttagga tcaggccaag aatcatctgg aaaacattat 1440
cttaattccg tctctcatat cctaaacagt acattttact aagaaattcc atatgaaaaa 1500
ctccactcat gtctcctgag attatcctgt aagtgaagta gctttcattt aaccaagcta 1560
aattatttcc atttagccat gttaaagaga agccaagtct agagaaagca atcctgtaac 1620
ccatgaatct ggtgtaccca ttttccctta acgtaacggg aagtgttttg aaattcccag 1680
aagagagctg ttttgtaatc aaagtgatgg attataagaa agccagactt tggaaaagga 1740
taattggaat aaagggaggt gcttgaagat tttccaaact actttatgtc atttagcttc 1800
tattttctga agggctttct ttgggtgcat gtactcagat cagtcagttg actgaaagat 1860
gatcatgttt tcttcgtaaa gatttaagca attggcaact acaaagacat tattttctta 1920
ctgttctata tcatgtactg ttgctgacat tacaaaaagg gtctggaagg gaaaccgtgt 1980
cactgtttta tcttttttct ttaaaatata aaagtatccc aactaatcat ttattatggg 2040
cagcttggtt tacatgtccc ctatgatgag aaatgctatc aacatctgtg atttctaaga 2100
gtcttaacca attgttactt taattcttgt gtccctgctga gtgggttttc ttttaaaata 2160
ccatttttat caccctgtgg cactgggtgt gttactgcga ttacactgat gattctgagc 2220
tgtgtctctt caagtagctc agttcttgcg ttttatatta ggtaacagtt ttgtgatgct 2280
tttgtgcatt ctttgtcatc tcttctgagt tttcgaatct gtcataaata aactttttca 2340
ctatgcacct ggtaaaaaa 2359
```

<210> 69

<211> 240

<212> DNA

<213> Homo sapiens

<400> 69

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cctaagccgc ctaagggggt gcctcggctg tccatcagtt acctcgtttc ctgagcagag 60
taattgggtg agattgttca tggaggcatt gctggctctc tagtcctgga acctacagtt 120
gggtccaatc attatgccaa agggctccgtc taggaggttc ttgttccaag tattgagatt 180
cccagagaaa gtaggtcccc ttagatagaa gcagagtttc tcagaggtat ttagcagcag 240
```

<210> 70

<211> 980

<212> DNA

<213> Homo sapiens

```

<400> 70
gccgctgccg ctccaggaga caggttccca tgcaggaatg aaagacatgg aaggggaagag 60
gggggccagc tccctgagtc ctgtgtccac cagctgctgc taaatacctc tgagaaactc 120
tgcttctatc taaggggacc tacttctctc ggggaatctca atacttggaa caagaacctc 180
ctagacggac cctttggcat aatgaattgg accaactgta ggttccagga ctagagagcc 240
agcaatgcct ccatgaacaa tctcacccaa ttactctgct caggaaacga ggtaactgat 300
ggacagccga ggcagccct taggcggctt aggcctcccc tgtggagcat ccctgaggcg 360
gactccggcc agcccagtg atgcatcca aagagcactc ccgggtagga aattgccccg 420
gtggaatgcc tcaccagagc agcgtgtagc agttccctgt ggaggattaa cacagtggct 480
gaacaccggg aaggaactgg cacttgaggt ccggacatct gaaacttgta gactgggagc 540
tgtacatgga tgggagcagc ttcaccaacc cctgcaaagt gactctgaag aagacgacaa 600
gccctgctcc agtcacacc ggaagctgac tgggtccacgc acagctgaag catgaggaaa 660
ctcatcgccg gactaatttt ccttaaaatt tagacttgca cagtaaggac ttcaactgac 720
cttcctcaga ctgagaactg tttccagtat atacatcaag tcaactgaggt aggacaaaag 780
attgctacat tcctattatt ttaaggttac atttttgggg acccctcttt cttctgttct 840
agctattacc tttctgtgt cacctagaaa aggaccagtc cttaattgta ttttaaaaac 900
tgtgatcatg ggaagcttta aattggttca ataacacgca tcaagttggt tatttcctgg 960
gctacatacc ttgatagat                                     980

```

```

<210> 71
<211> 118
<212> PRT
<213> Homo sapiens

```

```

<400> 71
Met Asp Ser Arg Gly Ser Pro Leu Gly Gly Leu Gly Leu Pro Cys Gly
 1             5             10             15

Ala Ser Leu Arg Arg Thr Pro Ala Ser Pro Ser Asp Ala Ile Gln Arg
      20             25             30

Ala Leu Pro Gly Arg Lys Leu Pro Arg Trp Asn Ala Ser Pro Glu Gln
 35             40             45

Arg Val Ala Val Pro Cys Gly Gly Leu Thr Gln Trp Leu Asn Thr Gly
 50             55             60

Lys Glu Leu Ala Leu Gly Val Arg Thr Ser Glu Thr Cys Arg Leu Gly
 65             70             75             80

Ala Val His Gly Trp Glu Gln Leu His Gln Pro Leu Gln Ser Asp Ser
      85             90             95

Glu Glu Asp Asp Lys Pro Cys Ser Ser His Thr Arg Lys Leu Thr Gly
100             105             110

Pro Arg Thr Ala Glu Ala
115

```

```

<210> 72
<211> 531
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> modified_base
<222> (519)
<223> n = g, a, c or t

```

```

<400> 72
aaaaaggtaa ttttcagcat tttggcacct aaaagggaaa ctttcatctg cttacacagg 60
ccagaagcaa agacaaagat tgcattgtgt tcttacagat gacttaaatc atctctttga 120
tgataaaaaat atttttaagc cgtgaaagtt atgagatatt ctgggtaagc ctgattatca 180
aagaatacca caaatagctt tggagatcgt gtattgtttg tcaactgagtc aaagagatct 240
gtgggattgt gaggattctt ggggtggagg gtgactaatc ctgcacgtcc ctttgtgaag 300
actccagtaa gtactcgcac aacgtacatg tgctttctcc cattgctgtc tggcttggag 360
taggtgtcct tggcagaata actggcatcc acagcaaaat aggttccttt tccataggat 420
acagcattttt tcccacacaa cttctattaa agccgtgctg attgacatat ggcactgagt 480
ctgcatctgt cccatggaag aggagtctct cattattcnt atggtcattc t 531

```

```

<210> 73
<211> 1956
<212> DNA
<213> Homo sapiens

```

```

<400> 73
attgttatca actctttgat atctgatgat caatgctcca aagaattgga ttaatatattt 60
tacacaatat tgtttagtgc agtaactgtt tctattttcca ggcatttttta gatgaattca 120
ctaactgggtc aagaataaat cccaacaagg ccaggattcc catggcagga gataccaag 180
gtgtgggtcgg gactgtctct aagccttgtt tcacagcata tgaaatgaaa atcgggtgcaa 240
ttacttttca ggttgtctact ggagatatag ccaactgaaca ggtagatgtt attgtaaact 300
caacagcaag gacatttaat cggaaatcag gtgtgtcaag agctatttta gaagggtgtg 360
gacaagctgt ggaaagtga tgtgctgtac tagctgcaca gcctcacaga gattttataa 420
ttacaccagg tggatgctta aagtgcāaaa taataattca tgttcctggg ggaaaagatg 480
tcaggaaaac ggtcaccagt gttctagaag agtgtgaaca gaggaagtac acatcggttt 540
cccttcagc cattggaaca ggaaatgccg gaaaaaaccc tatcacagtt gctgataaca 600
taatcgatgc tattgtagac ttctcatcac aacattccac cccatcatta aaaacagtta 660
aagttgtcat ttttcaacct gagctgctaa atatattcta cgacagcatg aaaaaaagag 720
acctctctgc atcactgaac tttcagtcca cattctccat gactacatgt aatcttctctg 780
aacactggac tgacatgaat catcagctgt tttgcatggg ccagctagag ccaggacaat 840
cagaatataa taccataaag gacaagttca cccgaacttg ttcttcctac gcaatagaga 900
agattgagag gatacagaat gcatttctct ggcagagcta ccaggtaaag aaaaggcaaa 960
tggatatcaa gaatgaccat aagaataatg agagactcct cttccatggg acagatgcag 1020
actcagtgcc atatgtcaat cagcacggct ttaatagaag ttgtgctggg aaaaatgctg 1080
tatectatgg aaaaggaacc tattttgctg tggatgccag ttattctgcc aaggacacct 1140
actccaagcc agacagcaat gggagaaagc acatgtacgt tgtgcgagta cttactggag 1200
tcttcacaaa gggacgtgca ggattagtca cccctccacc caagaatcct cacaatccca 1260
cagatctctt tgactcagtg acaaacaata cagcatctcc aaagctattt gtggtattct 1320
ttgataatca ggcttaccca gaatatctca taactttcac ggcttaaaaa tatttttatc 1380
atcaaagaga tgatttaagt catctgtaag aacaacatgc aatctttgtc tttgcttctg 1440
gcctgtgtaa gcagatgaaa gtttcccttt taggtgccaa aatgctgaaa attacctttt 1500
taaagtgtct tattgtctgc attttagtca tacctttttt tctcagcaaa ttgatgggtg 1560
gaagctgaga aatgtatggg aaatgtcaca gagctacaac cattcacaga caccaaactc 1620
ctaggagaat aaaaagcaca ttattctttt tctatcagaa aaaaacaaga tgcacacct 1680
taaaaccaag atgacattgt tcttcttgga acatgttaag acatcgaatg gtggcggtt 1740
aaactgtact gcttaagtgg agcggctacc gttatgcac tatcacagtt ggggattttg 1800
ccttattaag gaaaacttgt caatagttca gctgaaatga ctgaatcaca gaatattaac 1860
tctgttatgg aacaaatcat aacagatttt acctgtttac atttcaggta aaaatgtatc 1920
gcattgttat ctaatattaa aaaattaccc ccaatt 1956

```

```

<210> 74
<211> 444
<212> PRT
<213> Homo sapiens

```

```

<400> 74
Met Leu Gln Arg Ile Gly Leu Ile Phe Leu His Asn Ile Val Val Val
1 5 10 15

```



Ser Asn Cys Phe Tyr Phe Gln Ala Phe Leu Asp Glu Phe Thr Asn Trp  
 20 25 30  
 Ser Arg Ile Asn Pro Asn Lys Ala Arg Ile Pro Met Ala Gly Asp Thr  
 35 40 45  
 Gln Gly Val Val Gly Thr Val Ser Lys Pro Cys Phe Thr Ala Tyr Glu  
 50 55 60  
 Met Lys Ile Gly Ala Ile Thr Phe Gln Val Ala Thr Gly Asp Ile Ala  
 65 70 75 80  
 Thr Glu Gln Val Asp Val Ile Val Asn Ser Thr Ala Arg Thr Phe Asn  
 85 90 95  
 Arg Lys Ser Gly Val Ser Arg Ala Ile Leu Glu Gly Ala Gly Gln Ala  
 100 105 110  
 Val Glu Ser Glu Cys Ala Val Leu Ala Ala Gln Pro His Arg Asp Phe  
 115 120 125  
 Ile Ile Thr Pro Gly Gly Cys Leu Lys Cys Lys Ile Ile Ile His Val  
 130 135 140  
 Pro Gly Gly Lys Asp Val Arg Lys Thr Val Thr Ser Val Leu Glu Glu  
 145 150 155 160  
 Cys Glu Gln Arg Lys Tyr Thr Ser Val Ser Leu Pro Ala Ile Gly Thr  
 165 170 175  
 Gly Asn Ala Gly Lys Asn Pro Ile Thr Val Ala Asp Asn Ile Ile Asp  
 180 185 190  
 Ala Ile Val Asp Phe Ser Ser Gln His Ser Thr Pro Ser Leu Lys Thr  
 195 200 205  
 Val Lys Val Val Ile Phe Gln Pro Glu Leu Leu Asn Ile Phe Tyr Asp  
 210 215 220  
 Ser Met Lys Lys Arg Asp Leu Ser Ala Ser Leu Asn Phe Gln Ser Thr  
 225 230 235 240  
 Phe Ser Met Thr Thr Cys Asn Leu Pro Glu His Trp Thr Asp Met Asn  
 245 250 255  
 His Gln Leu Phe Cys Met Val Gln Leu Glu Pro Gly Gln Ser Glu Tyr  
 260 265 270  
 Asn Thr Ile Lys Asp Lys Phe Thr Arg Thr Cys Ser Ser Tyr Ala Ile  
 275 280 285  
 Glu Lys Ile Glu Arg Ile Gln Asn Ala Phe Leu Trp Gln Ser Tyr Gln  
 290 295 300  
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 Arg Leu Leu Phe His Gly Thr Asp Ala Asp Ser Val Pro Tyr Val Asn  
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Gln His Gly Phe Asn Arg Ser Cys Ala Gly Lys Asn Ala Val Ser Tyr  
340 345 350

Gly Lys Gly Thr Tyr Phe Ala Val Asp Ala Ser Tyr Ser Ala Lys Asp  
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Thr Tyr Ser Lys Pro Asp Ser Asn Gly Arg Lys His Met Tyr Val Val  
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Arg Val Leu Thr Gly Val Phe Thr Lys Gly Arg Ala Gly Leu Val Thr  
385 390 395 400

Pro Pro Pro Lys Asn Pro His Asn Pro Thr Asp Leu Phe Asp Ser Val  
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<212> PRT  
<213> Homo sapiens

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Pro Glu Asp Tyr Ile Ser Val Ile Gln Ser Ile Ile Phe Lys Asp Ser  
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Glu Asp Tyr Phe Glu Val Asn Ile Pro Thr Asp Leu Arg Ala Lys His  
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Ser Gly Glu Ile Ser Glu Arg Lys Glu Ile Glu Leu Ser Glu Ala  
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Ser Arg Asn Thr Ile Pro Leu Ala Val Val Leu Pro Thr Glu Ile Pro  
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 Cys Glu Asn Pro Gly Glu Ile Phe Ile Ile Leu Arg Asp Glu Val Ile  
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 <212> PRT  
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His	Val	Val	Lys	Arg	Glu	Ala	Ile	Leu	Leu	Tyr	Arg	Leu	Glu	Asn	Phe	
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Ser	Phe	Arg	His	Leu	Glu	Leu	Leu	Asn	Leu	Thr	Ser	Tyr	Lys	Cys	Lys	
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Pro	Gly	Glu	Ile	Phe	Ile	Ile	Leu	Arg	Asp	Glu	Val	Ile	Gly	Asp	Thr	
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Thr His Phe Lys Glu Leu Pro Thr Leu Leu His Cys Ala Ala Lys Phe  
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420 425 430  
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<212> PRT  
<213> Homo sapiens

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Phe Leu His Val Val Lys Arg Glu Ala Ile Leu Leu Tyr Arg Leu Glu
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Asn Phe Ser Phe Arg His Leu Glu Leu Leu Asn Leu Thr Ser Tyr Lys
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Cys Lys Leu Leu Ile Leu Ser Asn Ser Leu Leu Arg Asp Leu Thr Pro
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 Gly Glu Ile Ser Glu Arg Lys Glu Ile Glu Glu Leu Ser Glu Ala Ser  
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 Arg Asn Thr Ile Pro Leu Ala Val Val Leu Pro Thr Glu Ile Pro Cys  
 180 185 190  
 Glu Asp Pro Gly Glu Ile Phe Ile Ile Leu Arg Asp Glu Val Ile Gly  
 195 200 205  
 Asp Thr Val Glu Val Glu Phe Thr Ser Ser Asn Lys Arg Ile Arg Thr  
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 225 230 235 240  
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 245 250 255  
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 Pro Tyr Tyr Glu Phe Gln Ser Leu Gln Thr Glu Ile Cys Ser Gln Asn  
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Val Tyr Asn Lys Leu Thr Ile Val His His Pro Gly Gly Lys Glu Thr  
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Ala His Asn Glu Asn Lys Phe Tyr Asn Val His Phe Ser Asn Lys Leu  
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Asp His  
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<212> DNA  
<213> Homo sapiens

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<210> 97
<211> 2378
<212> DNA
<213> Homo sapiens

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<210> 98
<211> 313
<212> DNA
<213> Homo sapiens

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<223> n = g, a, c or t

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<211> 317
<212> DNA
<213> Homo sapiens

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<210> 100  
 <211> 1968  
 <212> DNA  
 <213> Homo sapiens

<400> 100

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 <211> 486  
 <212> PRT  
 <213> Homo sapiens

<400> 101

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Glu	Lys	Glu	Gln	Arg	Trp	Gly	Ala	Lys	Thr	Ile	Glu	Gly	Ser	Gly	Arg
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 His Asp Val Leu Arg Lys Lys Glu Met Glu Ser Gly Pro Lys Ala Ser  
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 His Gly Tyr Gly Gly Arg Phe Gly Val Glu Arg Asp Arg Met Asp Lys  
 85 90 95  
 Ser Ala Val Gly His Glu Tyr Val Ala Glu Val Glu Lys His Ser Ser  
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 Gln Thr Asp Ala Ala Lys Gly Phe Gly Gly Lys Tyr Gly Val Glu Arg  
 115 120 125  
 Asp Arg Ala Asp Lys Ser Ala Val Gly Phe Asp Tyr Lys Gly Glu Val  
 130 135 140  
 Glu Lys His Thr Ser Gln Lys Asp Tyr Ser Arg Gly Phe Gly Gly Arg  
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 Tyr Gly Val Glu Lys Asp Lys Trp Asp Lys Ala Ala Leu Gly Tyr Asp  
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 Tyr Lys Gly Glu Thr Glu Lys His Glu Ser Gln Arg Asp Tyr Ala Lys  
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 Gly Phe Gly Gly Gln Tyr Gly Ile Gln Lys Asp Arg Val Asp Lys Ser  
 195 200 205  
 Ala Val Gly Phe Asn Glu Met Glu Ala Pro Thr Thr Ala Tyr Lys Lys  
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 Thr Thr Pro Ile Glu Ala Ala Ser Ser Gly Ala Arg Gly Leu Lys Ala  
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 260 265 270  
 Lys Arg Ser Pro Glu Ala Pro Gln Pro Val Ile Ala Met Glu Glu Pro  
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 Pro Val Gly Thr Pro Pro Ser Ser Glu Ser Glu Pro Val Arg Thr Ser  
 305 310 315 320  
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 Asp Asn Glu Glu Pro Pro Ala Leu Pro Pro Arg Thr Leu Glu Gly Leu  
 340 345 350  
 Gln Val Glu Glu Glu Pro Val Tyr Glu Ala Glu Pro Glu Pro Glu Pro  
 355 360 365

Glu Pro Glu Pro Glu Pro Glu Asn Asp Tyr Glu Asp Val Glu Glu Met  
 370 375 380

Asp Arg His Glu Gln Glu Asp Glu Pro Glu Gly Asp Tyr Glu Glu Val  
 385 390 395 400

Leu Glu Pro Glu Asp Ser Ser Phe Ser Ser Ala Leu Ala Gly Ser Ser  
 405 410 415

Gly Cys Pro Ala Gly Ala Gly Ala Gly Ala Val Ala Leu Gly Ile Ser  
 420 425 430

Ala Val Ala Leu Tyr Asp Tyr Gln Gly Glu Gly Ser Asp Glu Leu Ser  
 435 440 445

Phe Asp Pro Asp Asp Val Ile Thr Asp Ile Glu Met Val Asp Glu Gly  
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Tyr Val Lys Leu Leu Glu  
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 <212> DNA  
 <213> Homo sapiens

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 <212> DNA  
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<210> 104  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

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Asp Ser Gly Leu Ala Gln Arg Arg Phe Ile Arg Gly Trp Gly Leu Cys  
           35                          40                          45  
 Ile Phe Leu Pro Phe Val Leu Ser Gln Leu Glu Pro Gly Cys Lys Lys  
           50                          55                          60  
 Glu Leu Pro Glu Phe Glu Gly Asp Val Leu Ala Val Gly Ser Gln Ala  
           65                          70                          75                          80  
 Leu Thr Thr Glu Gly Ile Tyr Glu Asp Val Ile Arg Gly Cys Leu Leu  
                           85                          90                          95  
 Gln Arg Ile Asp Gln Glu Leu Lys Lys Thr Leu Gly Ala Asn Asp Val  
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 <211> 5107  
 <212> DNA  
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<210> 107

<211> 579

<212> PRT

<213> Homo sapiens

<400> 107

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His Leu Arg Gly Gln Val Asp Thr Leu Leu Arg Asn Phe Leu Pro Cys  
 35 40 45

Tyr Arg Gly Gln Leu Ala Ala Ser Val Leu Arg Gln Ile Ser Arg Glu  
 50 55 60

Leu Gly Pro Gln Glu Pro Thr Gly Ser Gln Leu Leu Arg Ser Lys Lys  
 65 70 75 80

Leu Pro Arg Val Arg Glu His Arg Gly Pro Leu Thr Gln Leu Arg Gly  
 85 90 95

His Pro Pro Arg Trp Gln Pro Ile Phe Cys Val Leu Arg Gly Asp Gly  
 100 105 110

Arg Leu Glu Trp Phe Ser His Lys Glu Glu Tyr Glu Asn Gly Gly His  
 115 120 125

Cys Leu Gly Ser Thr Ala Leu Thr Gly Tyr Thr Leu Leu Thr Ser Gln  
 130 135 140

Arg Glu Tyr Leu Arg Leu Leu Asp Ala Leu Cys Pro Glu Ser Leu Gly  
 145 150 155 160

Asp His Thr Gln Glu Glu Pro Asp Ser Leu Leu Glu Val Pro Val Ser  
 165 170 175

Phe Pro Leu Phe Leu Gln His Pro Phe Arg Arg His Leu Cys Phe Ser  
 180 185 190

Ala Ala Thr Arg Glu Ala Gln His Ala Trp Arg Leu Ala Leu Gln Gly  
 195 200 205

Gly Ile Arg Leu Gln Gly Thr Val Leu Gln Arg Ser Gln Ala Pro Ala  
 210 215 220

Ala Arg Ala Phe Leu Asp Ala Val Arg Leu Tyr Arg Gln His Gln Gly  
 225 230 235 240



His Phe Gly Asp Asp Val Thr Leu Gly Ser Asp Ala Glu Val Leu  
 245 250 255  
 Thr Ala Val Leu Met Arg Glu Gln Leu Pro Ala Leu Arg Ala Gln Thr  
 260 265 270  
 Leu Pro Gly Leu Arg Gly Ala Gly Arg Ala Arg Ala Trp Ala Trp Thr  
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 Glu Leu Leu Asp Ala Val His Ala Ala Val Leu Ala Gly Ala Ser Ala  
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 Gly Leu Cys Ala Phe Gln Pro Glu Lys Asp Glu Leu Leu Ala Ser Leu  
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 Glu Lys Thr Ile Arg Pro Asp Val Asp Gln Leu Leu Arg Gln Arg Ala  
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 Arg Val Ala Gly Arg Leu Arg Thr Asp Ile Arg Gly Pro Leu Glu Ser  
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 Cys Leu Arg Arg Glu Val Asp Pro Gln Leu Pro Arg Val Val Gln Thr  
 355 360 365  
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 370 375 380  
 Ala Gln Gly Met Asp Arg Leu Ser His Arg Leu Arg Gln Ser Pro Ser  
 385 390 395 400  
 Gly Thr Arg Leu Arg Arg Glu Val Tyr Ser Phe Gly Glu Met Pro Trp  
 405 410 415  
 Asp Leu Ala Leu Met Gln Thr Cys Tyr Arg Glu Ala Glu Arg Ser Arg  
 420 425 430  
 Gly Arg Leu Gly Gln Leu Ala Ala Pro Phe Gly Phe Leu Gly Met Gln  
 435 440 445  
 Ser Leu Val Phe Gly Ala Gln Asp Leu Ala Gln Gln Leu Met Ala Asp  
 450 455 460  
 Ala Val Ala Thr Phe Leu Gln Leu Ala Asp Gln Cys Leu Thr Thr Ala  
 465 470 475 480  
 Leu Asn Cys Asp Gln Ala Ala Gln Arg Leu Glu Arg Val Arg Gly Arg  
 485 490 495  
 Val Leu Lys Lys Phe Lys Ser Asp Ser Gly Leu Ala Gln Arg Arg Phe  
 500 505 510  
 Ile Arg Gly Trp Gly Leu Cys Ile Phe Leu Pro Phe Val Leu Ser Gln  
 515 520 525  
 Leu Glu Pro Gly Cys Lys Lys Thr Glu Ser Arg Ser Val Ala Gln Ala  
 530 535 540  
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Phe Lys Arg Ser Ser His Leu Gly Leu Pro Ser Ser Trp Asp Tyr Arg  
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His Pro Leu

<210> 108  
<211> 2917  
<212> DNA  
<213> Homo sapiens

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 <211> 83  
 <212> PRT  
 <213> Homo sapiens

<400> 109  
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 Ser Leu Gln Ser Ser Trp Asp Tyr Arg His Ala Pro Pro Arg Pro Ala  
 35 40 45  
 Asn Phe Val Phe Leu Val Glu Thr Gly Phe Cys His Val Ser Gln Ala  
 50 55 60  
 Gly Leu Glu Leu Leu Thr Ser Ser Asp Pro Pro Pro Arg Pro Pro Lys  
 65 70 75 80  
 Val Leu Arg

<210> 110  
 <211> 509  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (467)  
 <223> n = g, a, c or t

<400> 110  
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 cataaaaaga aatgttcaat gtttctagaa gacaaataat tacaaaccta aacaaattgt 420  
 atatttgta gattggcata aattataata atccaacatt gagttangtg gaatataaat 480  
 tggtaaaata tttctggaag acaatttgg 509

<210> 111  
 <211> 525  
 <212> DNA  
 <213> Homo sapiens

<400> 111  
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 ggtaccagat gatgataata tatctgaaaa cacaagccat ttttattctt tatcccaatt 420  
 aacttgaggt actctaata tgaagcactc gattgcacta tgacctcctt gagtgatggg 480  
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<210> 112  
 <211> 183  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1)..(183)  
 <223> n = g, a, c or t

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 ttgactttgg actgtanaag cttttctttg atcacctgtg ntggaggaaa ggaaagaagc 180  
 ctt 183

<210> 113  
 <211> 1750  
 <212> DNA  
 <213> Homo sapiens

<400> 113  
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 gtggagcccc agaaccctgt gctctctgct ggagggtccc tgtttgtgaa ctgcagtact 180  
 gattgtccca gctctgagaa aatcgccttg gagacgtccc tatcaaagga gctgggtggcc 240  
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 aaaaaaaaaa 1750

<210> 114  
 <211> 547  
 <212> PRT  
 <213> Homo sapiens

<400> 114

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			20					25					30		
Leu	Leu	Arg	Val	Glu	Pro	Gln	Asn	Pro	Val	Leu	Ser	Ala	Gly	Gly	Ser
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Leu	Phe	Val	Asn	Cys	Ser	Thr	Asp	Cys	Pro	Ser	Ser	Glu	Lys	Ile	Ala
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Leu	Glu	Thr	Ser	Leu	Ser	Lys	Glu	Leu	Val	Ala	Ser	Gly	Met	Gly	Trp
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Ala	Ala	Phe	Asn	Leu	Ser	Asn	Val	Thr	Gly	Asn	Ser	Arg	Ile	Leu	Cys
				85					90					95	
Ser	Val	Tyr	Cys	Asn	Gly	Ser	Gln	Ile	Thr	Gly	Ser	Ser	Asn	Ile	Thr
			100					105					110		
Val	Tyr	Gly	Leu	Pro	Glu	Arg	Val	Glu	Leu	Ala	Pro	Leu	Pro	Pro	Trp
		115					120					125			
Gln	Pro	Val	Gly	Gln	Asn	Phe	Thr	Leu	Arg	Cys	Gln	Val	Glu	Gly	Gly
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Leu	Ser	Arg	Gln	Pro	Ala	Val	Glu	Glu	Pro	Ala	Glu	Val	Thr	Ala	Thr
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Val	Leu	Ala	Ser	Arg	Asp	Asp	His	Gly	Ala	Pro	Phe	Ser	Cys	Arg	Thr
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Glu	Leu	Asp	Met	Gln	Pro	Gln	Gly	Leu	Gly	Leu	Phe	Val	Asn	Thr	Ser
		195					200					205			
Ala	Pro	Arg	Gln	Leu	Arg	Thr	Phe	Val	Leu	Pro	Val	Thr	Pro	Pro	Arg
	210					215					220				
Leu	Val	Ala	Pro	Arg	Phe	Leu	Glu	Val	Glu	Thr	Ser	Trp	Pro	Val	Asp
225					230					235					240
Cys	Thr	Leu	Asp	Gly	Leu	Phe	Pro	Ala	Ser	Glu	Ala	Gln	Val	Tyr	Leu
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			260					265					270		
Thr	Leu	Thr	Ala	Thr	Ala	Thr	Ala	Thr	Ala	Arg	Ala	Asp	Gln	Glu	Gly
		275					280					285			
Ala	Arg	Glu	Ile	Val	Cys	Asn	Val	Thr	Leu	Gly	Gly	Glu	Arg	Arg	Glu
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Leu Ser Glu Pro Thr Ala His Glu Gly Ser Thr Val Thr Val Ser Cys  
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 Met Ala Gly Ala Arg Val Gln Val Thr Leu Asp Gly Val Pro Ala Ala  
 340 345 350  
 Ala Pro Gly Gln Pro Ala Gln Leu Gln Leu Asn Ala Thr Glu Ser Asp  
 355 360 365  
 Asp Gly Arg Ser Phe Phe Cys Ser Ala Thr Leu Glu Val Asp Gly Glu  
 370 375 380  
 Phe Leu His Arg Asn Ser Ser Val Gln Leu Arg Val Leu Tyr Gly Pro  
 385 390 395 400  
 Lys Ile Asp Arg Ala Thr Cys Pro Gln His Leu Lys Trp Lys Asp Lys  
 405 410 415  
 Thr Arg His Val Leu Gln Cys Gln Ala Arg Gly Asn Pro Tyr Pro Glu  
 420 425 430  
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 435 440 445  
 Pro Phe Phe Val Asn Val Thr His Asn Gly Thr Tyr Gln Cys Gln Ala  
 450 455 460  
 Ser Ser Ser Arg Gly Lys Tyr Thr Leu Val Val Val Met Asp Ile Glu  
 465 470 475 480  
 Ala Gly Ser Ser His Phe Val Pro Val Phe Val Ala Val Leu Leu Thr  
 485 490 495  
 Leu Gly Val Val Thr Ile Val Leu Ala Leu Met Tyr Val Phe Arg Glu  
 500 505 510  
 His Gln Arg Ser Gly Ser Tyr His Val Arg Glu Glu Ser Thr Tyr Leu  
 515 520 525  
 Pro Leu Thr Ser Met Gln Pro Thr Glu Ala Met Gly Glu Glu Pro Ser  
 530 535 540  
 Arg Ala Glu  
 545

<210> 115  
 <211> 275  
 <212> DNA  
 <213> Homo sapiens

<400> 115  
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 cgatactcag gccatgaagt acttgtcata cctgctgtac cctctctgtg tcgggggtgc 120  
 tgtctattca ctctgaata tcaaataaa gagctggtag tcctgggtta tcaacagctt 180  
 cgtcaacggg gtctatgcct ttggtttcct cttcatgctg cccagctct ttgtgaacta 240  
 caagttgaag tcagtggcac atctgcctg gaagg 275

<210> 116  
 <211> 2040  
 <212> DNA  
 <213> Homo sapiens

<400> 116  
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 ggtcatgtac ggcacgtct acaccgccc gtgctccggc gacgccaact gcatccagcc 120  
 ctacctggcg cggcgcccca agctgcagct gagcgtgtac accacgacga ggtcccacct 180  
 ggggtgctgag aacaacatcg acctggtctt gaatgtggaa gactttgatg tggagtccaa 240  
 atttgaaagg acagttaatg tttctgtacc aaagaaaacg agaaacaatg ggacgctgta 300  
 tgcctacatc ttcctccatc acgtgggggt cctgccgtgg cagcagggga agcaggtgca 360  
 cctggtcagt cctctgacca cctacatggg ccccaagcca gaagaaatca acctgctcac 420  
 cggggagtct gatacacagc agatcgaggc ggagaagaag ccgacgagtg ccctggatga 480  
 gccagtgtcc cactggcgac cgcggctggc gctgaacgtg atggcggaca actttgtctt 540  
 tgacgggtcc tccctgcctg ccgatgtgca tcggtacatg aagatgatcc agctggggaa 600  
 aaccgtgcat tacctgcccc tcctgttcat cgaccagctc agcaaccgcg tgaaggacct 660  
 gatggtcata aaccgctcca ccaccgagct gcccctcacc gtgtcctacg acaaggcttc 720  
 actggggcgg ctgcgcttct ggatccaat gcaggacgcc gtgtactccc tgcagcagtt 780  
 cgggttttca gagaaagatg ctgatgaggt gaaaggaatt tttgtagata ccaacttata 840  
 cttcctggcg ctgaccttct ttgtcgcagc gttccatctt ctctttgatt tcctggcctt 900  
 taaaaatgac atcagtttct ggaagaagaa gaagagcatg atcggcatgt ccaccaaggc 960  
 agtgcctctg cgctgcttca gcaccgtggg catctttctg ttcctgctgg acgagcagac 1020  
 gagcctgctg gtgctggtcc cggcgggtgt tggagccgcc attgagctgt ggaaagtga 1080  
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 cctcttcacg ctgccccagc tctttgtgaa ctacaagttg aagtcagtgg cacatctgcc 1380  
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 ctacctgtac cagcgggtggc tttatcctgt ggataaacgc agagtgaacg agtttgggga 1560  
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 gccagccaag tgcaacttga attgtcaatg agtatctttg gaagcatttg gaggaattcc 1680  
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 gttcccatca cgtcagattt ggagctggta gcgcttacga tgccccacg tgtgaacatc 1800  
 tgtcttggtc acagagctgg gtgctgccgg tcaccttgag ctgtggtggc tcccggcaca 1860  
 cgagtgtccg ggggttcggc atgtcctcac gcgggcaggg gtggggagccc tcacaggcaa 1920  
 gggggctggt ggatttccat ttcaggtggg ttcttaagtg ctcttatgt gaatttcaaa 1980  
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<210> 117  
 <211> 538  
 <212> PRT  
 <213> Homo sapiens

<400> 117  
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 Thr Arg Pro Cys Ser Gly Asp Ala Asn Cys Ile Gln Pro Tyr Leu Ala  
 35 40 45  
 Arg Arg Pro Lys Leu Gln Leu Ser Val Tyr Thr Thr Arg Ser His  
 50 55 60

Leu Gly Ala Glu Asn Asn Ile Asp Leu Val Leu Asn Val Glu Asp Phe  
 65 70 75 80  
 Asp Val Glu Ser Lys Phe Glu Arg Thr Val Asn Val Ser Val Pro Lys  
 85 90 95  
 Lys Thr Arg Asn Asn Gly Thr Leu Tyr Ala Tyr Ile Phe Leu His His  
 100 105 110  
 Ala Gly Val Leu Pro Trp His Asp Gly Lys Gln Val His Leu Val Ser  
 115 120 125  
 Pro Leu Thr Thr Tyr Met Val Pro Lys Pro Glu Glu Ile Asn Leu Leu  
 130 135 140  
 Thr Gly Glu Ser Asp Thr Gln Gln Ile Glu Ala Glu Lys Lys Pro Thr  
 145 150 155 160  
 Ser Ala Leu Asp Glu Pro Val Ser His Trp Arg Pro Arg Leu Ala Leu  
 165 170 175  
 Asn Val Met Ala Asp Asn Phe Val Phe Asp Gly Ser Ser Leu Pro Ala  
 180 185 190  
 Asp Val His Arg Tyr Met Lys Met Ile Gln Leu Gly Lys Thr Val His  
 195 200 205  
 Tyr Leu Pro Ile Leu Phe Ile Asp Gln Leu Ser Asn Arg Val Lys Asp  
 210 215 220  
 Leu Met Val Ile Asn Arg Ser Thr Thr Glu Leu Pro Leu Thr Val Ser  
 225 230 235 240  
 Tyr Asp Lys Val Ser Leu Gly Arg Leu Arg Phe Trp Ile His Met Gln  
 245 250 255  
 Asp Ala Val Tyr Ser Leu Gln Gln Phe Gly Phe Ser Glu Lys Asp Ala  
 260 265 270  
 Asp Glu Val Lys Gly Ile Phe Val Asp Thr Asn Leu Tyr Phe Leu Ala  
 275 280 285  
 Leu Thr Phe Phe Val Ala Ala Phe His Leu Leu Phe Asp Phe Leu Ala  
 290 295 300  
 Phe Lys Asn Asp Ile Ser Phe Trp Lys Lys Lys Lys Ser Met Ile Gly  
 305 310 315 320  
 Met Ser Thr Lys Ala Val Leu Trp Arg Cys Phe Ser Thr Val Val Ile  
 325 330 335  
 Phe Leu Phe Leu Leu Asp Glu Gln Thr Ser Leu Leu Val Leu Val Pro  
 340 345 350  
 Ala Gly Val Gly Ala Ala Ile Glu Leu Trp Lys Val Lys Lys Ala Leu  
 355 360 365  
 Lys Met Thr Ile Phe Trp Arg Gly Leu Met Pro Glu Phe Gln Phe Gly  
 370 375 380



Thr Tyr Ser Glu Ser Glu Arg Lys Thr Glu Glu Tyr Asp Thr Gln Ala  
 385 390 395 400  
 Met Lys Tyr Leu Ser Tyr Leu Leu Tyr Pro Leu Cys Val Gly Gly Ala  
 405 410 415  
 Val Tyr Ser Leu Leu Asn Ile Lys Tyr Lys Ser Trp Tyr Ser Trp Leu  
 420 425 430  
 Ile Asn Ser Phe Val Asn Gly Val Tyr Ala Phe Gly Phe Leu Phe Met  
 435 440 445  
 Leu Pro Gln Leu Phe Val Asn Tyr Lys Leu Lys Ser Val Ala His Leu  
 450 455 460  
 Pro Trp Lys Ala Phe Thr Tyr Lys Ala Phe Asn Thr Phe Ile Asp Asp  
 465 470 475 480  
 Val Phe Ala Phe Ile Ile Thr Met Pro Thr Ser His Arg Leu Ala Cys  
 485 490 495  
 Phe Arg Asp Asp Val Val Phe Leu Val Tyr Leu Tyr Gln Arg Trp Leu  
 500 505 510  
 Tyr Pro Val Asp Lys Arg Arg Val Asn Glu Phe Gly Glu Ser Tyr Glu  
 515 520 525  
 Glu Lys Ala Thr Arg Ala Pro His Thr Asp  
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<210> 118  
 <211> 4217  
 <212> DNA  
 <213> Homo sapiens

<400> 118  
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 gcacaagaag cccttccttg ccaaataactt cccctttatg gacctgaagc tccgagcagc 180  
 ctccccgatc attacattgg tggcccttga tgaagccctt gacaactaca ccatcacatt 240  
 cctcatccgc ggtgtggcca tcggccagac cagtctaact gcaagtgtga ccaataaagc 300  
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 gccaggaag gtgacactgc ttatcggggc cagcatgcag gtcacctccg agggcgggcc 420  
 ccagcctcag tccaacatcc ttttctccat cagcaatgag agcgttgccg tggtgagcgc 480  
 tgctgggctg gtacagggcc tcgccatcgg gaacggcact gtgtctgggc tcgtgcaggc 540  
 agtggatgca gagaccgga aggtggtcat catctctcag gacctcgtgc aggtggagg 600  
 gctgctgcta agggccgtga ggatccgcgc ccccatcatg cggatgagga cgggcaccca 660  
 gatgccccatc tatgtcaccg gcatcaccaa ccaccagaac cctttctcct ttggcaatgc 720  
 cgtgccaggc ctgaccttcc actggtctgt caccaagcgg gacgtcctgg acctccgagg 780  
 gcggcaccac gaggcgtcga tccgactccc gtcacagtac aactttgcca tgaacgtgct 840  
 cggccgggta aaaggccgga ccgggctgag ggtggtggtc aaggctgtgg accccacatc 900  
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 gaagctgcag ctgctcaacc ctgaaataga agcagaacaa atattaatgt cgcccaactc 1020  
 atatataaag ctgcagacaa acagggatgg tgcagcctct ctgagctacc gcgtcctgga 1080  
 tggaccggaa aagggttccag ttgtgcatgt tgatgagaaa ggctttctag catcaggggtc 1140  
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 catcattggt gctgttaaagg tatccctgtg ttccctacctg agggtttcca tgagccctgt 1260  
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 cactgtccac ttccacgaca actctggaga tgtcttccat gctcacagtt cggctcctcaa 1380  
 ctttgccact aacagagacg actttgtgca gatcgggaag ggccccacca acaacacctg 1440

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<210> 119

<211> 923

<212> PRT

<213> Homo sapiens

<400> 119

Phe	Pro	Ala	Pro	Ala	Lys	Ala	Val	Val	Tyr	Val	Ser	Asp	Ile	Gln	Glu
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Leu	Tyr	Ile	Arg	Val	Val	Asp	Lys	Val	Glu	Ile	Gly	Lys	Thr	Val	Lys
			20						25					30	

Ala Tyr Val Arg Val Leu Asp Leu His Lys Lys Pro Phe Leu Ala Lys  
 35 40 45  
 Tyr Phe Pro Phe Met Asp Leu Lys Leu Arg Ala Ala Ser Pro Ile Ile  
 50 55 60  
 Thr Leu Val Ala Leu Asp Glu Ala Leu Asp Asn Tyr Thr Ile Thr Phe  
 65 70 75 80  
 Leu Ile Arg Gly Val Ala Ile Gly Gln Thr Ser Leu Thr Ala Ser Val  
 85 90 95  
 Thr Asn Lys Ala Gly Gln Arg Ile Asn Ser Ala Pro Gln Gln Ile Glu  
 100 105 110  
 Val Phe Pro Pro Phe Arg Leu Met Pro Arg Lys Val Thr Leu Leu Ile  
 115 120 125  
 Gly Ala Thr Met Gln Val Thr Ser Glu Gly Gly Pro Gln Pro Gln Ser  
 130 135 140  
 Asn Ile Leu Phe Ser Ile Ser Asn Glu Ser Val Ala Leu Val Ser Ala  
 145 150 155 160  
 Ala Gly Leu Val Gln Gly Leu Ala Ile Gly Asn Gly Thr Val Ser Gly  
 165 170 175  
 Leu Val Gln Ala Val Asp Ala Glu Thr Gly Lys Val Val Ile Ile Ser  
 180 185 190  
 Gln Asp Leu Val Gln Val Glu Val Leu Leu Leu Arg Ala Val Arg Ile  
 195 200 205  
 Arg Ala Pro Ile Met Arg Met Arg Thr Gly Thr Gln Met Pro Ile Tyr  
 210 215 220  
 Val Thr Gly Ile Thr Asn His Gln Asn Pro Phe Ser Phe Gly Asn Ala  
 225 230 235 240  
 Val Pro Gly Leu Thr Phe His Trp Ser Val Thr Lys Arg Asp Val Leu  
 245 250 255  
 Asp Leu Arg Gly Arg His His Glu Ala Ser Ile Arg Leu Pro Ser Gln  
 260 265 270  
 Tyr Asn Phe Ala Met Asn Val Leu Gly Arg Val Lys Gly Arg Thr Gly  
 275 280 285  
 Leu Arg Val Val Val Lys Ala Val Asp Pro Thr Ser Gly Gln Leu Tyr  
 290 295 300  
 Gly Leu Ala Arg Glu Leu Ser Asp Glu Ile Gln Val Gln Val Phe Glu  
 305 310 315 320  
 Lys Leu Gln Leu Leu Asn Pro Glu Ile Glu Ala Glu Gln Ile Leu Met  
 325 330 335  
 Ser Pro Asn Ser Tyr Ile Lys Leu Gln Thr Asn Arg Asp Gly Ala Ala  
 340 345 350

Ser Leu Ser Tyr Arg Val Leu Asp Gly Pro Glu Lys Val Pro Val Val  
 355 360 365  
 His Val Asp Glu Lys Gly Phe Leu Ala Ser Gly Ser Met Ile Gly Thr  
 370 375 380  
 Ser Thr Ile Glu Val Ile Ala Gln Glu Pro Phe Gly Ala Asn Gln Thr  
 385 390 395 400  
 Ile Ile Val Ala Val Lys Val Ser Pro Val Ser Tyr Leu Arg Val Ser  
 405 410 415  
 Met Ser Pro Val Leu His Thr Gln Asn Lys Glu Ala Leu Val Ala Val  
 420 425 430  
 Pro Leu Gly Met Thr Val Thr Phe Thr Val His Phe His Asp Asn Ser  
 435 440 445  
 Gly Asp Val Phe His Ala His Ser Ser Val Leu Asn Phe Ala Thr Asn  
 450 455 460  
 Arg Asp Asp Phe Val Gln Ile Gly Lys Gly Pro Thr Asn Asn Thr Cys  
 465 470 475 480  
 Val Val Arg Thr Val Ser Val Gly Leu Thr Leu Leu Arg Val Trp Asp  
 485 490 495  
 Ala Glu His Pro Gly Leu Ser Asp Phe Met Pro Leu Pro Val Leu Gln  
 500 505 510  
 Ala Ile Ser Pro Glu Leu Ser Gly Ala Met Val Val Gly Asp Val Leu  
 515 520 525  
 Cys Leu Ala Thr Val Leu Thr Ser Leu Glu Gly Leu Ser Gly Thr Trp  
 530 535 540  
 Ser Ser Ser Ala Asn Ser Ile Leu His Ile Asp Pro Lys Thr Gly Val  
 545 550 555 560  
 Ala Val Ala Arg Ala Val Gly Ser Val Thr Val Tyr Tyr Glu Val Ala  
 565 570 575  
 Gly His Leu Arg Thr Tyr Lys Glu Val Val Val Ser Val Pro Gln Arg  
 580 585 590  
 Ile Met Ala Arg His Leu His Pro Ile Gln Thr Ser Phe Gln Glu Ala  
 595 600 605  
 Thr Ala Ser Lys Val Ile Val Ala Val Gly Asp Arg Ser Ser Asn Leu  
 610 615 620  
 Arg Gly Glu Cys Thr Pro Thr Gln Arg Glu Val Ile Gln Ala Leu His  
 625 630 635 640  
 Pro Glu Thr Leu Ile Ser Cys Gln Ser Gln Phe Lys Pro Ala Val Phe  
 645 650 655  
 Asp Phe Pro Ser Gln Asp Val Phe Thr Val Glu Pro Gln Phe Asp Thr  
 660 665 670

Ala Leu Gly Gln Tyr Phe Cys Ser Ile Thr Met His Arg Leu Thr Asp  
 675 680 685  
 Lys Gln Arg Lys His Leu Ser Met Lys Lys Thr Ala Leu Val Val Ser  
 690 695 700  
 Ala Ser Leu Ser Ser Ser His Phe Ser Thr Glu Gln Val Gly Ala Glu  
 705 710 715 720  
 Val Pro Phe Ser Pro Gly Leu Phe Ala Asp Gln Ala Glu Ile Leu Leu  
 725 730 735  
 Ser Asn His Tyr Thr Ser Ser Glu Ile Arg Val Phe Gly Ala Pro Glu  
 740 745 750  
 Val Leu Glu Asn Leu Glu Val Lys Ser Gly Ser Pro Ala Val Leu Ala  
 755 760 765  
 Phe Ala Lys Glu Lys Ser Phe Gly Trp Pro Ser Phe Ile Thr Tyr Thr  
 770 775 780  
 Val Gly Val Ser Asp Pro Ala Ala Gly Ser Gln Gly Pro Leu Ser Thr  
 785 790 795 800  
 Thr Leu Thr Phe Ser Ser Pro Val Thr Asn Gln Ala Ile Ala Ile Pro  
 805 810 815  
 Val Thr Val Ala Phe Val Met Asp Arg Arg Gly Pro Gly Pro Tyr Gly  
 820 825 830  
 Ala Ser Leu Phe Gln His Phe Leu Asp Ser Tyr Gln Val Met Phe Phe  
 835 840 845  
 Thr Leu Phe Ala Leu Leu Ala Gly Thr Ala Val Met Ile Ile Ala Tyr  
 850 855 860  
 His Thr Val Cys Thr Pro Arg Asp Leu Ala Val Pro Ala Ala Leu Thr  
 865 870 875 880  
 Pro Arg Ala Ser Pro Gly His Ser Pro His Tyr Phe Ala Ala Ser Ser  
 885 890 895  
 Pro Thr Ser Pro Asn Ala Leu Pro Pro Ala Arg Lys Ala Ser Pro Pro  
 900 905 910  
 Ser Gly Leu Trp Ser Pro Ala Tyr Ala Ser His  
 915 920

<210> 120

<211> 1270

<212> PRT

<213> Homo sapiens

<400> 120

Arg Asp Phe Gln Ser Glu Val Leu Leu Ser Ala Met Glu Leu Phe His  
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 20 25 30

Gln Pro Ser Ala Glu Ala Ala Ala Pro Ser Leu Ala Asn Ile Ser  
 35 40 45  
 Cys Phe Thr Gln Lys Leu Val Glu Lys Leu Tyr Ser Gly Met Phe Ser  
 50 55 60  
 Ala Asp Pro Arg His Ile Leu Leu Phe Ile Leu Glu His Ile Met Val  
 65 70 75 80  
 Val Ile Glu Thr Ala Ser Ser Gln Arg Asp Thr Val Leu Ser Thr Leu  
 85 90 95  
 Tyr Ser Ser Leu Asn Lys Val Ile Leu Tyr Cys Leu Ser Lys Pro Gln  
 100 105 110  
 Gln Ser Leu Ser Glu Cys Leu Gly Leu Leu Ser Ile Leu Gly Phe Leu  
 115 120 125  
 Gln Glu His Trp Asp Val Val Phe Ala Thr Tyr Asn Ser Asn Ile Ser  
 130 135 140  
 Phe Leu Leu Cys Leu Met His Cys Leu Leu Leu Leu Asn Glu Arg Ser  
 145 150 155 160  
 Tyr Pro Glu Gly Phe Gly Leu Glu Pro Lys Pro Arg Met Ser Thr Tyr  
 165 170 175  
 His Gln Val Phe Leu Ser Pro Asn Glu Asp Val Lys Glu Lys Arg Glu  
 180 185 190  
 Asp Leu Pro Ser Leu Ser Asp Val Gln His Asn Ile Gln Lys Thr Val  
 195 200 205  
 Gln Thr Leu Trp Gln Gln Leu Val Ala Gln Arg Gln Gln Thr Leu Glu  
 210 215 220  
 Asp Ala Phe Lys Ile Asp Leu Ser Val Lys Pro Gly Glu Arg Glu Val  
 225 230 235 240  
 Lys Ile Glu Glu Val Thr Pro Leu Trp Glu Glu Thr Met Leu Lys Ala  
 245 250 255  
 Trp Gln His Tyr Leu Ala Ser Glu Lys Lys Ser Leu Ala Ser Arg Ser  
 260 265 270  
 Asn Val Ala His His Ser Lys Val Thr Leu Trp Ser Gly Ser Leu Ser  
 275 280 285  
 Ser Ala Met Lys Leu Met Pro Gly Arg Gln Ala Lys Asp Pro Glu Cys  
 290 295 300  
 Lys Thr Glu Asp Phe Val Ser Cys Ile Glu Asn Tyr Arg Arg Arg Gly  
 305 310 315 320  
 Gln Glu Leu Tyr Ala Ser Leu Tyr Lys Asp His Val Gln Arg Arg Lys  
 325 330 335  
 Cys Gly Asn Ile Lys Ala Ala Asn Ala Trp Ala Arg Ile Gln Glu Gln  
 340 345 350

Leu Phe Gly Glu Leu Gly Leu Trp Ser Gln Gly Glu Glu Thr Lys Pro  
 355 360 365  
 Cys Ser Pro Trp Glu Leu Asp Trp Arg Glu Gly Pro Ala Arg Met Arg  
 370 375 380  
 Lys Arg Ile Lys Arg Leu Ser Pro Leu Glu Ala Leu Ser Ser Gly Arg  
 385 390 395 400  
 His Lys Glu Ser Gln Asp Lys Asn Asp His Ile Ser Gln Thr Asn Ala  
 405 410 415  
 Glu Asn Gln Asp Glu Leu Thr Leu Arg Glu Ala Glu Gly Glu Pro Asp  
 420 425 430  
 Glu Val Gly Val Asp Cys Thr Gln Leu Thr Phe Phe Pro Ala Leu His  
 435 440 445  
 Glu Ser Leu His Ser Glu Asp Phe Leu Glu Leu Cys Arg Glu Arg Gln  
 450 455 460  
 Val Ile Leu Gln Glu Leu Leu Asp Lys Glu Lys Val Thr Gln Lys Phe  
 465 470 475 480  
 Ser Leu Val Ile Val Gln Gly His Leu Val Ser Glu Gly Val Leu Leu  
 485 490 495  
 Phe Gly His Gln His Phe Tyr Ile Cys Glu Asn Phe Thr Leu Ser Pro  
 500 505 510  
 Thr Gly Asp Val Tyr Cys Thr Arg His Cys Leu Ser Asn Ile Ser Asp  
 515 520 525  
 Pro Phe Ile Phe Asn Leu Cys Ser Lys Asp Arg Ser Thr Asp His Tyr  
 530 535 540  
 Ser Cys Gln Cys His Ser Tyr Ala Asp Met Arg Glu Leu Arg Gln Ala  
 545 550 555 560  
 Arg Phe Leu Leu Gln Asp Ile Ala Leu Glu Ile Phe Phe His Asn Gly  
 565 570 575  
 Tyr Ser Lys Phe Leu Val Phe Tyr Asn Asn Asp Arg Ser Lys Ala Phe  
 580 585 590  
 Lys Ser Phe Cys Ser Phe Gln Pro Ser Leu Lys Gly Lys Ala Thr Ser  
 595 600 605  
 Glu Asp Thr Leu Asn Leu Arg Arg Tyr Pro Gly Ser Asp Arg Ile Met  
 610 615 620  
 Leu Gln Lys Trp Gln Lys Arg Asp Ile Ser Asn Phe Glu Tyr Leu Met  
 625 630 635 640  
 Tyr Leu Asn Thr Ala Ala Gly Arg Thr Cys Asn Asp Tyr Met Gln Tyr  
 645 650 655  
 Pro Val Phe Pro Trp Val Leu Ala Asp Tyr Thr Ser Glu Thr Leu Asn  
 660 665 670

Leu Ala Asn Pro Lys Ile Phe Arg Asp Leu Ser Lys Pro Met Gly Ala  
 675 680 685  
 Gln Thr Lys Glu Arg Lys Leu Lys Phe Ile Gln Arg Phe Lys Glu Val  
 690 695 700  
 Glu Lys Thr Glu Gly Asp Met Thr Val Gln Cys His Tyr Tyr Thr His  
 705 710 715 720  
 Tyr Ser Ser Ala Ile Ile Val Ala Ser Tyr Leu Val Arg Met Pro Pro  
 725 730 735  
 Phe Thr Gln Ala Phe Cys Ala Leu Gln Gly Gly Ser Phe Asp Val Ala  
 740 745 750  
 Asp Arg Met Phe His Ser Val Lys Ser Thr Trp Glu Ser Ala Ser Arg  
 755 760 765  
 Glu Asn Met Ser Asp Val Arg Glu Leu Thr Pro Glu Phe Phe Tyr Leu  
 770 775 780  
 Pro Glu Phe Leu Thr Asn Cys Asn Gly Val Glu Phe Gly Cys Met Gln  
 785 790 795 800  
 Asp Gly Thr Val Leu Gly Asp Val Gln Leu Pro Pro Trp Ala Asp Gly  
 805 810 815  
 Asp Pro Arg Lys Phe Ile Ser Leu His Arg Lys Ala Leu Glu Ser Asp  
 820 825 830  
 Phe Val Ser Ala Asn Leu His His Trp Ile Asp Leu Ile Phe Gly Tyr  
 835 840 845  
 Lys Gln Gln Gly Pro Ala Ala Val Asp Ala Val Asn Ile Phe His Pro  
 850 855 860  
 Tyr Phe Tyr Gly Asp Arg Met Asp Leu Ser Ser Ile Thr Asp Pro Leu  
 865 870 875 880  
 Ile Lys Ser Thr Ile Leu Gly Phe Val Ser Asn Phe Gly Gln Val Pro  
 885 890 895  
 Lys Gln Leu Phe Thr Lys Pro His Pro Ala Arg Thr Ala Ala Gly Lys  
 900 905 910  
 Pro Leu Pro Gly Lys Asp Val Ser Thr Pro Val Ser Leu Pro Gly His  
 915 920 925  
 Pro Gln Pro Phe Phe Tyr Ser Leu Gln Ser Leu Arg Pro Ser Gln Val  
 930 935 940  
 Thr Val Lys Asp Met Tyr Leu Phe Ser Leu Gly Ser Glu Ser Pro Lys  
 945 950 955 960  
 Gly Ala Ile Gly His Ile Val Ser Thr Glu Lys Thr Ile Leu Ala Val  
 965 970 975  
 Glu Arg Asn Lys Val Leu Leu Pro Pro Leu Trp Asn Arg Thr Phe Ser  
 980 985 990



Trp Gly Phe Asp Asp Phe Ser Cys Cys Leu Gly Ser Tyr Gly Ser Asp  
 995 1000 1005  
 Lys Val Leu Met Thr Phe Glu Asn Leu Ala Ala Trp Gly Arg Cys Leu  
 1010 1015 1020  
 Cys Ala Val Cys Pro Ser Pro Thr Thr Ile Val Thr Ser Gly Thr Ser  
 1025 1030 1035 1040  
 Thr Val Val Cys Val Trp Glu Leu Ser Met Thr Lys Gly Arg Pro Arg  
 1045 1050 1055  
 Gly Leu Arg Leu Arg Gln Ala Leu Tyr Gly His Thr Gln Ala Val Thr  
 1060 1065 1070  
 Cys Leu Ala Ala Ser Val Thr Phe Ser Leu Leu Val Ser Gly Ser Gln  
 1075 1080 1085  
 Asp Cys Thr Cys Ile Leu Trp Asp Leu Asp His Leu Thr His Val Thr  
 1090 1095 1100  
 Arg Leu Pro Ala His Arg Glu Gly Ile Ser Ala Ile Thr Ile Ser Asp  
 1105 1110 1115 1120  
 Val Ser Gly Thr Ile Val Ser Cys Ala Gly Ala His Leu Ser Leu Trp  
 1125 1130 1135  
 Asn Val Asn Gly Gln Pro Leu Ala Ser Ile Thr Thr Ala Trp Gly Pro  
 1140 1145 1150  
 Glu Gly Ala Ile Thr Cys Cys Cys Leu Met Glu Gly Pro Ala Trp Asp  
 1155 1160 1165  
 Thr Ser Gln Ile Ile Ile Thr Gly Ser Gln Asp Gly Met Val Arg Val  
 1170 1175 1180  
 Trp Lys Thr Glu Asp Val Lys Met Ser Val Pro Gly Arg Pro Ala Gly  
 1185 1190 1195 1200  
 Glu Glu Pro Leu Ala Gln Pro Pro Ser Pro Arg Gly His Lys Trp Glu  
 1205 1210 1215  
 Lys Asn Leu Ala Leu Ser Arg Glu Leu Asp Val Ser Ile Ala Leu Thr  
 1220 1225 1230  
 Gly Lys Pro Ser Lys Thr Ser Pro Ala Val Thr Ala Leu Ala Val Ser  
 1235 1240 1245  
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<211> 647

<212> PRT

<213> Homo sapiens

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 Tyr Pro Val Phe Pro Trp Val Leu Ala Asp Tyr Thr Ser Glu Thr Leu  
 35 40 45  
 Asn Leu Ala Asn Pro Lys Ile Phe Arg Asp Leu Ser Lys Pro Met Gly  
 50 55 60  
 Ala Gln Thr Lys Glu Arg Lys Leu Lys Phe Ile Gln Arg Phe Lys Glu  
 65 70 75 80  
 Val Glu Lys Thr Glu Gly Asp Met Thr Val Gln Cys His Tyr Tyr Thr  
 85 90 95  
 His Tyr Ser Ser Ala Ile Ile Val Ala Ser Tyr Leu Val Arg Met Pro  
 100 105 110  
 Pro Phe Thr Gln Ala Phe Cys Ala Leu Gln Gly Gly Ser Phe Asp Val  
 115 120 125  
 Ala Asp Arg Met Phe His Ser Val Lys Ser Thr Trp Glu Ser Ala Ser  
 130 135 140  
 Arg Glu Asn Met Ser Asp Val Arg Glu Leu Thr Pro Glu Phe Phe Tyr  
 145 150 155 160  
 Leu Pro Glu Phe Leu Thr Asn Cys Asn Gly Val Glu Phe Gly Cys Met  
 165 170 175  
 Gln Asp Gly Thr Val Leu Gly Asp Val Gln Leu Pro Pro Trp Ala Asp  
 180 185 190  
 Gly Asp Pro Arg Lys Phe Ile Ser Leu His Arg Lys Ala Leu Glu Ser  
 195 200 205  
 Asp Phe Val Ser Ala Asn Leu His His Trp Ile Asp Leu Ile Phe Gly  
 210 215 220  
 Tyr Lys Gln Gln Gly Pro Ala Ala Val Asp Ala Val Asn Ile Phe His  
 225 230 235 240  
 Pro Tyr Phe Tyr Gly Asp Arg Met Asp Leu Ser Ser Ile Thr Asp Pro  
 245 250 255  
 Leu Ile Lys Ser Thr Ile Leu Gly Phe Val Ser Asn Phe Gly Gln Val  
 260 265 270  
 Pro Lys Gln Leu Phe Thr Lys Pro His Pro Ala Arg Thr Ala Ala Gly  
 275 280 285  
 Lys Pro Leu Pro Gly Lys Asp Val Ser Thr Pro Val Ser Leu Pro Gly  
 290 295 300  
 His Pro Gln Pro Phe Phe Tyr Ser Leu Gln Ser Leu Arg Pro Ser Gln  
 305 310 315 320

Val Thr Val Lys Asp Met Tyr Leu Phe Ser Leu Gly Ser Glu Ser Pro  
325 330 335  
Lys Gly Ala Ile Gly His Ile Val Ser Thr Glu Lys Thr Ile Leu Ala  
340 345 350  
Val Glu Arg Asn Lys Val Leu Leu Pro Pro Leu Trp Asn Arg Thr Phe  
355 360 365  
Ser Trp Gly Phe Asp Asp Phe Ser Cys Cys Leu Gly Ser Tyr Gly Ser  
370 375 380  
Asp Lys Val Leu Met Thr Phe Glu Asn Leu Ala Ala Trp Gly Arg Cys  
385 390 395 400  
Leu Cys Ala Val Cys Pro Ser Pro Thr Thr Ile Val Thr Ser Gly Thr  
405 410 415  
Ser Thr Val Val Cys Val Trp Glu Leu Ser Met Thr Lys Gly Arg Pro  
420 425 430  
Arg Gly Leu Arg Leu Arg Gln Ala Leu Tyr Gly His Thr Gln Ala Val  
435 440 445  
Thr Cys Leu Ala Ala Ser Val Thr Phe Ser Leu Leu Val Ser Gly Ser  
450 455 460  
Gln Asp Cys Thr Cys Ile Leu Trp Asp Leu Asp His Leu Thr His Val  
465 470 475 480  
Thr Arg Leu Pro Ala His Arg Glu Gly Ile Ser Ala Ile Thr Ile Ser  
485 490 495  
Asp Val Ser Gly Thr Ile Val Ser Cys Ala Gly Ala His Leu Ser Leu  
500 505 510  
Trp Asn Val Asn Gly Gln Pro Leu Ala Ser Ile Thr Thr Ala Trp Gly  
515 520 525  
Pro Glu Gly Ala Ile Thr Cys Cys Cys Leu Met Glu Gly Pro Ala Trp  
530 535 540  
Asp Thr Ser Gln Ile Ile Ile Thr Gly Ser Gln Asp Gly Met Val Arg  
545 550 555 560  
Val Trp Lys Thr Glu Asp Val Lys Met Ser Val Pro Gly Arg Pro Ala  
565 570 575  
Gly Glu Glu Pro Leu Ala Gln Pro Pro Ser Pro Arg Gly His Lys Trp  
580 585 590  
Glu Lys Asn Leu Ala Leu Ser Arg Glu Leu Asp Val Ser Ile Ala Leu  
595 600 605  
Thr Gly Lys Pro Ser Lys Thr Ser Pro Ala Val Thr Ala Leu Ala Val  
610 615 620

Ser Arg Asn His Thr Lys Leu Leu Val Gly Asp Glu Arg Gly Arg Ile  
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Phe Cys Trp Ser Ala Asp Gly  
 645

<210> 122

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR  
 amplification primer PDM-797

<400> 122

gtgtcacaat ctacagtcag gcaggattct cc

32

<210> 123

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR  
 amplification primer PDM-799

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gttatgtagc ggccgcttat catgttgctg cagag

35

<210> 124

<211> 980

<212> DNA

<213> Homo sapiens

<400> 124

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 tgctttctatc taaggggacc tacttctctc gggaatctca atacttgga caagaacctc 180  
 ctagacggac cctttggcat aatgaattgg accaactgta ggttccagga ctagagagcc 240  
 agcaatgcct ccatgaacaa tctcacccaa ttactctgct caggaaacga ggtaactgat 300  
 ggacagccga ggcagcccct taggcggctt aggcctcccc tgtggagcat ccctgaggcg 360  
 gactccggcc agcccgagt atgcatcca aagagcactc ccgggtagga aattgccccg 420  
 gtggaatgcc tcaccagagc agcgtgtagc agttccctgt ggaggattaa cacagtggct 480  
 gaacaccggg aagggaactg cacttgaggc ccggacatct gaaacttgta gactgggagc 540  
 tgtacatgga tgggagcagc ttcaccaacc cctgcaaagt gactctgaag aagacgacaa 600  
 gccctgctcc agtcacaccc ggaagctgac tgggtccacgc acagctgaag catgaggaaa 660  
 ctcatcgcg gactaatttt ccttaaaatt tagacttgca cagtaaggac ttcaactgac 720  
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 gctacatacc ttggatagat 980

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